## STIC-Biotech/ChemLib

144232

From:

Whiteman, Brian

Sent:

Monday, August 29, 2005 4:04 PM

To:

STIC-Biotech/ChemLib

Subject:

seq search

09/801,371

SEQ ID NO: 1 and 2

1) the commercial databases, and the issued and published US application databases

Thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

STAFF USE ONLY

Searcher:
Searcher Phone: 2Date Searcher Picked up
Date Completed:
Searcher Prep/Rev. Time:
Online Time:

Type of Search

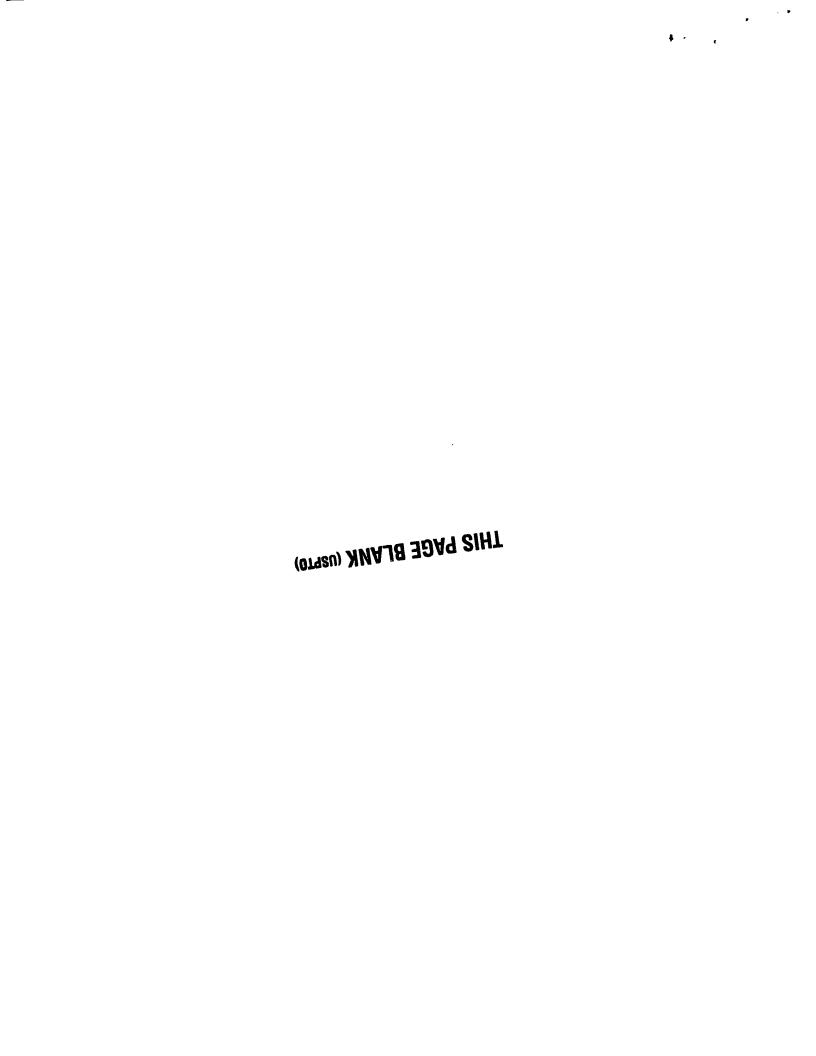
Vendors and cost where applicable STN:\_\_\_\_\_

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DIALOG:\_\_\_\_\_\_\_QUESTEL/ORBIT:\_\_\_\_\_\_

LEXIS/NEXIS:
SEQUENCE SYSTEM: 402
WWW/Internet:

Other(Specify):\_\_



BCC028148 Homo Bapi BD137687 Self-regu AR300459 Sequence BD137688 Self-regu AR300460 Sequence AR100270 Sequence BD237798 AntiBense BD27739 AntiBense BD2771232 Predictio BD664008 Novel exp XC02910 Human gene AX0066019 Homo Bapi AX100955 Sequence AX100955 Sequence AX100955 Sequence AX100955 Sequence AX100955 Sequence AX100959 Sequence AX224167 Human DNA AX22597 Sequence BX348519 Human DNA AL9229587 Human DNA

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G13533 400 bp DNA linear STS 30-MAR-2000 SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site.
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1. (bases 1 to 400)

Olivier, M. and Cox, D.R.

Unpublished, Olivier, M., Cox, D.R. (2000)
                                                                                                                                                                                                                                                                                                                                                                                  Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 94025, USA
Tel: (650) 320-5801
Fax: (650) 320-5801
Email: olivier@shgc.stanford.edu
Primer A: CACTAAGAATTCAAACTGGGGC
Primer B: GAGGAAGGCCTAAGGTCCAC
STS size: 166
                       AR300459
AR300460
HUMTNFX
AR100270
AR100270
AR10027798
BD227798
BD227798
BD227798
AY066019
AX100950
HUMTNFA
AX100955
HUMTNFABX
AX562497
HXSTNFABX
BX248519
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Polymerization:
PCR Cycles:
Thermal Cycler:
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Homo sapiens
1000.00
Protocol:
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G13533 SHGC-11076
BD137681 Self-regu
AR310453 Sequence
BD070551 Self-regu
108430 Sequence 5
107953 Sequence 6
E00702 CDNA encodi
103510 Sequence 2
10444 Sequence 2
A37272 Sequence 12
104198 Sequence 1
104198 Sequence 1
108384 Sequence 1
108429 Sequence 3
AR380784 Sequence 22
AR36225 Sequence 22
                                                     2, 2005, 18:55:28; Search time 1896.05 Seconds (without alignments) 2657.805 Million cell updates/sec
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                                                                                                      1 gaattcaaaactggggcctcc......ggttctggccagaatgctgc 104
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                                                                                                                                                               9416466
      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                              4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                      nucleic search, using sw model
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AR366225
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94 degrees C for 1 62 degrees C for 2 72 degrees C for 3 30 Perkin Elmer 9600

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PAT 12-JUN-2003

linear

104

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bDUγO551 787 bp DNA linear PAT 27-AUG-2002
Self-regulated apoptosis of inflammatory cells by gene therapy.
BD070551
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I (bases 1 to 787)

S Tatake, R.J., Marlin, S.D. and Barton, R.W.

S Tatake, R.J., Marlin, S.D. and Barton, R.W.

Self-regulated apoptosis of inflammatory cells by gene therapy

L patent: JP 2001516210-A 13 25-SEP-2001;

BOCHRINGER INGELHEIM PHARMACEUTICALS INC

DN JP 2001516210-A/13

PD 25-SEP-2001

PP 25-SEP-1998 JP 1998537909

PR 28-FEB-1999 US 60/039266

PI REVATI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC

A61131/70, COOTA21/04, C12N15/12, C12P19/34

CC Strandedness: Single;

CC TOPOLOGY: Linear;

CC TNF alpha nontranslated region

FT SOURCE

L'NF Alpha nontranslated region

L'Organism='Unidentified'.
1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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Tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: US 6537784 A 7 25-WAR-2003;
Location/Qualifiers
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AR300453
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/mol_type="genomic DNA"
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JP 2001516210-A/13.
unidentified
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1 (Dases 1 to 787)
Tatake,R.J.; Marlin,S.D. and Barton,R.W.
Tatake,R.J.; Marlin,S.D. and Earton,R.W.
Paelf-regulated apoptosis of inflammatory cells by gene therapy Patent: JP 2002504381-A 7 12-FEB-2002;
BOEHRINGER INGELHEIM PHARMACEUTICALS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Location/Qualifiers
1. .787
/organism="Homo sapiens"
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/organism="Homo sapiens"
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/map="6"
                                                                                                                                                                                                                                                                                                                                    /clone_lib="Human"
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210. .231
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JP 2002504381-A/7.
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VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL FEATURES

ORIGIN

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OS homosapiens
PN 19 196040221-A/1
PD 26-FEB-1986
05-JUL-1985 JP 1985149075
PR 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 677156, PR 03-DEC-1984 US 84 677156, PR BUSHIYAN AGAAWARU, DEBITSUDO BANNOOMAN GETSUDERU, PI SAN HII RII, PI GURBN EBAN NEDOUIN
PC AGIKIS/12, AGIKIS/02, AGIKIS/14, AGIKIS/74, AGIKIS/102, AGIKI
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1 (bases 1 to 1324)
Baraa,B.A., Debitsudo,B.G., San,H.R. and Guren,E.N.

TUMOR NECTROTIC FACTOR

Patent: JP 1986040221-A 1 26-FEB-1986;
                                                                                                     750 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                     1 GAATICAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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/product='tumor necrosis factor' FT
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                                                                                                                                                       61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                                                                                                                                                                  810 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 853
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     0; Indels
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*source: cell_line=HL-60;
*source: clone=lambda42-4;
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                                                                                                                                                                                                                                                                                                                          cDNA encoding human tumor necrosis factor.
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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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topology: Linear;
hypothetical: No;
anti-sense: No;
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JP 1986040221-A/1.
Homo sapiens (human)
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Unknown.
Unclassified.
I (bases 1 to 1323)
Aggarwal, B.B., Lee, S.H., Goeddel, D.V. and Nedwin, G.E.
Aggarwal, B.B., Lee, S.H., and Deckling it, DNA encoding it and assay method using such DNA
Patent: EP 0168214-A2 6 15-JAN-1986;
Location/Qualifiers
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Mark.D.F., Lin.L.S., Lu,S.-D.Y. and Wang,A.M.
CYSTSINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR PROTEINS
PATENT: WO 8604606-A 5 14-AUG-1986;
Location/Qualifiers
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tive 0; Mismatches 0;
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al Similarity 100.0%; Score 104; Call Similarity 100.0%; Pred. No. 1.3
104; Conservative 0; Mismatches

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/organism="unknown"
/mol_type="unassigned DNA"

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Sequence 6 from Patent EP 0168214.
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Sequence 5 from Patent WO 8604606.
/db_xref="taxon:32644"
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Lin,L.S. and Yamamoto,R.
Purification method for tunor necrosis factor
Parent: US 4677197-A 2 30-UIN-1987;
Cetus Corporation; Emeryville, CA
Location/Qualifiers
                                                                                                                                                                                                                                                                                     100.0%; Score 104; DB 6;
100.0%; Pred. No. 1.3e-24;
iive 0; Mismatches 0;
                              1324 bp ss-DNA
Sequence 2 from Patent US 4650674.
103610
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Sequence 2 from Patent US 4677197,
104244
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Aggarwal, B. B. and Lee, S.He.
Synergistic cytotoxic composition
Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco,
Location/Qualifiers

    .1465
/organism="unknown"
/mol_type="unassigned DNA"

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DEFINITION Sequence 12 from Patent WO9404196.
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/organism="unknown"
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Matches 104; Conservative
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1 (bases 1 to 1585)
Mark,D.F., Wang,A.M., Ladner,M.B., Creasey,A.A., Lin,L.S. and Van
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Sequence 1 from Patent US 4677063.
104169
                                                                  unclassified
unclassified.
1 (bases 1 to 1585)
Vile,R.G. and Hart,I.R.
TUMOUR THERAPY
Patent: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
Location/Qualifiers
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Sequence 1 from Patent US 4677064.
104198
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Patent: US 4677063-A 1 30-JUN-1987;
Cetus Corporation; Emeryville, CA
GI:2294369
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Search completed: September 3, 2005, 01:14:20
Job time : 1902.05 secs
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AR380784
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TITLE
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KEYWORDS
SOURCE
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Mark, D.F., Wang, A.M., Ladner, M.B., Creasey, A.A., Lin, L.S. and Van Asdell, J.N.
HUMAN TUMOR NECROSIS FACTOR
Patent: WO 8602381-A 5 24-APR-1986;
Location/Qualifiers
1. 1585
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                                       1 (bases 1 to 1585)
Mark, D.E., Wang, A.M., Ladner, M.B., Creasey, A.A., Van Arsdell, J.N. and Lin, L.S.
Human tumor necrosis factor
Patent: 103 4677064-A 130-JUN-1987;
Cetus Corporation; Emeryville, CA
Location/Qualifiers
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Sequence 5 from Patent WO 8602381.
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1 (bases 1 to 1585)
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Best Local Similarity 100.
Matches 104; Conservative
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              Unknown.
Unclassified.
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I08429
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1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACACTTG 1062
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Unclassified.
1 (bases 1 to 1585)
Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Cockspoiltions for the detection of blood cell and immunological cresponse gene expression
Patent: US 6607879-A 1329 19-AUG-2003;
                                                                                                                                                                                                                                                                                                               1 GAATICAAACIGGGGCCTCCAGAACICACIGGGGCCTIACAGCTITGAICCCIGACAICIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG
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Mark, D.F., Lin, L.S., Lu, S.-D.Y. and Wang, A.M.
CYSTEINE-DEPETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR PROTEINS
Patent: W0 8604666.A 3 14-AUG-1986;
Location/Qualifiers
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; Pred. No. 1.3e-24;
0; Mismatches 0;
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Sequence 1329 from patent US 6607879.
AR380784
AR380784.1 GI:40088418
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100.0%;
Best Local Similarity 100.0%;
Matches 104; Conservative 0
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87

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AAZ99816 standard; RNA; 104
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                                                                                                        3; Search time 319.075 Seconds (without alignments) 1929.494 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                        September 2, 2005, 18:45:43
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaz99816 Cis-actin	Aaz20979 Human TNF	Adr12297 Human tum	Aan60558 Sequence	Aan60363 Sequence	Aaa34963 Human ade	Aaf21085 Human low	Abz96779 Human nuc	Abd20628 Human pul	Aan80219 Sequence	Adq83817 Human tum	Aan60557 Seguence	Aca64836 Human TNF	Adf76346 Novel hum	Adi32003 Human cDN	Ado19587 Human PRO	Adr24640 Breast ca	Adp54654 Human PRO	Aan60446 Sequence	Aat15424 Human tum
SUMMARIES	ΩI	AAZ99816	AAZ20979	ADR12297	AAN60558	AAN60363	AAA34963	AAF21085	ABZ96779	ABD20628	AAN80219	ADQ83817	AAN60557	ACA64836	ADF76346	AD132003	ADO19587	ADR24640	ADP54654	AAN60446	AAT15424
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	Score	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104
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Aat31021 Human tum	Abk13195 Human tum	Aal53712 Tumour ne	Aad49644 Human tum	Adc35185 Human cDN	Aad63904 Human TNF	Acc57575 Polynucle	Adr26040 Breast ca	Acf64375 Human INF	Ade25664 Human cDN	Ad888038 Tumour tr	Adt08160 Human tum	Aaz20983 Chimeric	Aaz20984 Chimeric	Aav39005 TNF-alpha	Aax09014 Tumour ne	Aaa40760 Human tum	Aac63770 Human TNF	Acc57891 Human tum	Aca64946 Human TNF	Acd04988 DNA encod	Acf63382 Human TNF	Adq29070 Human tum	Adro2586 Human tum	Acf57523 Human TNF
2 AAT31021	9	8	8 AAD49644	10 ADC35185	10	10	13 ADR26040	8 ACF64375	10 ADE25664	13	• •	7	7	7	2 AAX09014	3 AAA40760	3 AAC63770	8 ACC57891	8 ACA64946	9 ACD04988	10 ACF63382	12 ADQ29070	13 ADR02586	12 ACF57523
1643	1643	1643	1643	1643	1643	1643	1643	1650	1666	1669	1669	2270	2570	3634	3634	3634	3634	3634	3634	3634	3634	3634	3634	4830
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104	104
21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

BP

(first entry)

The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic Regulation of gene expression by mRNA splicing is carried out using a cis -acting nucleotide sequence controlled by phosphorylation of the alphasubunit of eukaryotic initiation factor 2. Cis-acting sequence, intron removal, trans-acting factor; alpha-subunit; RNA-activated protein kinase, eukaryotic initiation factor 2; eIF2alpha; tumour necrosis factor alpha; TNF-alpha; gene therapy; ss. Cis-acting nucleotide sequence derived from human TNF-alpha. Ben-Asouli Y; Jarrous N, Claim 4; Page 15; 75pp; English. 99WO-IL000483. 98IL-00126112. 98IL-00126757. (YISS ) YISSUM RES & DEV CO. Kaempfer R, Osman F, WPI; 2000-257000/22. WO200014255-A1. 06-SEP-1999; 07-SEP-1998; 26-OCT-1998; Ното варіепв 16-MAR-2000. 

apoptosis. Pharmaceutical compositions of the chimeric nucleotide

undergo

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initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNP-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The
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                                                                                                                                                               protein) or industrially or agriculturally expression or industrially or agriculture of the present sequence of the
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                                                                                                                                                                                                                                                                              Score 104; DB 3; Length 104;
Pred. No. 3.1e-25;
0; Mismatches 0; Indels (
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100.0%;
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                                                                                                                                                                                                                                                                                                                        Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tatake RJ, Marlin SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human TNFalpha 3'UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527630/44.
                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JAN-1999;
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                                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
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Identifying modulators of untranslated region-dependent expression of a WEGF gene, useful for treating cancer, comprises contacting a compound with a cell or translation mixture containing a reporter gene linked to a VEGF gene UTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A method of identifying (MI) a compound that modulates untranslated region-dependent expression of a vascular endothelial growth factor (VEGF) gene comprises contacting a member of a library of compounds with a cell or cell-free translation mixture containing a reporter gene operably linked to an untranslated region (UTR) of the VEGF gene, and detecting expression of the reporter gene. A compound is identified as modulator if the level of expression of the reporter gene in the presence of the compound is altered as compared to that in the absence of the compound or in the presence of a control. Compounds identified by MI are useful for treating, preventing or ameliorating cancer or its symptoms, and/or for inhibiting angiogenesis. This sequence corresponds to a therapeutic untranslated region used in the invention.
                                                                                                                                                                                                                                                                                                                             GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 281
                                                                                                                                                                                                                                                                                                    9
                                       versus
                may be useful for treating inflammatory disorders such as multiple sclenosis, crohi's disease, ulcerative colitis, psoriasis, graft versus host disease, lupus erythematosus, insulin-dependent (type I) diabetes mellitus, ankylosing spondylitis, and in particular, rheumatoid arthritis. The use of such chimeric nucleotides offers simpler and chaper long-term relief, in comparison with existing conventional pharmaceutical and invasive surgery methods
                                                                                                                                                                                                                                                                                                    1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGGTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                              Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour necrosis factor alpha 3'-untranslated region DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    вв; сутовтатіс; VEGF modulator; angiogeneвів inhibitor;
UTR-dependent expression; vascular endothelial growth factor;
                                                                                                                                                                                                                     100.0%; Score 104; DB 2; Length 787; 100.0%; Pred. No. 5.4e-25;
                                                                                                                                                                               Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325
                                                                                                                                                                                                                                                                                                                                                                                 104
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                   GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC
                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              untranslated region; cancer; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; SEQ ID NO 6; 251pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
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                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-571681/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR12297;
                                                                                                                                                                                                                                                                                                                                            222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 3
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RESULT 4 AAN60558 AAN60558;

Key

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693 GAATICAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encodes the pure human tumour necrosis factor, mutants of which are covered by the claims. TNF and mutants are useful in treating tumours, especially in trandem with interferon. The encoding sequence may be used to create plasmid pTrpXAPINF, allowing transformation of an E.coli host for the expression of TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pure tumour necrosis factor and mutant forms - new DNA coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;
                                                             GAATCTGGAGGCCATTTGGTTCTGGCCAGAATGCTGC
                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/label= Secretory leader peptide
61. .534
/*tag= c
                                                                                                                                                                                                                                            Sequence encoding human tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nedwin GE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                              Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goeddel DV,
                                                                                                                                                                                                                                                                             cancer; interferon;
                                GAATCTGGAGACCAGGGAGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Fig 10; 90pp; English.
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84US-00628060.
84US-00677156.
84US-00677257.
84US-00677267.
                                                                                                                                               AAN60363 standard; DNA; 1323
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P-PSDB; AAP60417.
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                                                                                                                                                                                                                                                                           hTNF; tumour;
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05-JUL-1984;
03-DEC-1984;
03-DEC-1984;
03-DEC-1984;
                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                              19-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
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                                                                                                                                          219 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 278
                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New synthetic muteins of human tumour necrosis factor protein - are obtd.
by direct mutagenesis and retain antitumour activity.
                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser
                                                                                                           1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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                                              Length 792;
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           Sequence 792 BP; 192 A; 203 C; 172 G; 225 T; 0 U; 0 Other;
                                                                                                                                                                       GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                                                            Indels
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                                              DB 13;
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                                            Query Match
100.0%; Score 104; DB 13;
Best Local Similarity 100.0%; Pred. No. 5.4e-25;
Matches 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 3a; 47pp; English.
                                                                                                                                                                                                                                                                                       AAN60558 standard; DNA; 1275 BP
                                          100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Antitumour; anticancer; ss
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P-PSDB; AAP60656.
                                                                                                                                                                                                                                                                                                                                                                                                           in pAW731.
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Mark DF,

ö 9 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG Gapa ° Length 1323; 0; Indels 100.0%; Score 104; DB 1; 100.0%; Pred. No. 6.2e-25; ઠે

61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104

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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c. impaired airways, including lung disease subdiseases syndrome, pain, cystic impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive certinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the convented said effects. The A-containing ONs break down with the conchoconstriction and inflammation. AAA3313 to AAA3331 represent the invention, which correspond to SEQ ID NO:1 to 185, but the sequences differ sequences are also called SEQ ID NO:1 to 185, but the sequence of from the previously named sequences. SEQ ID NO:1 to 185, but the sequence of from the previously named sequences. SEQ ID NO:1 to 180 (AAA3333 to AAA3392) are specifically claimed ONs from the present invention. N B. Sequences given in the disclosure of the present invention. N B. Sequences given in the sequence given in the sequence in the sequence of the present invention. We sequence is the present invention. N B. Sequences given in the sequence of the present invention. We sequence is the present invention. We sequence the present invention to the sequence of the present invention. We sequence the present invention to the sequence of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adenosine receptor related polynucleotide SEQ ID NO:2652.
cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 814-815; 1343pp; English.
                                                                                                                                                                                                                                                                                                               AAA34963 standard; DNA; 1324 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                   AAA34963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              listing
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Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

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Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                         751 GAATICAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810
                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; pulmonary distriction; asthma; RDS; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonuclectides and compositions (I) comprising them. In the antisense oligonuclectides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiniflammatory, analgesic, immunosuppressive, antisathmatic, hypotensive and cytostatic activities. The antisense oligonuclectides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide
                                                                                   GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGGCTTACAGCTTTGATCCCTGACATCTG
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human low adenosine antisense oligonucleotide related sequence #2652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes low adenosine (A) content antisense
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Length 1324;
                                                                                                                                                                                         811 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 854
                                                                                                                                                                 61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                        0; Indels
  Score 104; DB 3;
Pred. No. 6.2e-25;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 887; 1592pp; English.
                                                                                                                                                                                                                                                                                                            AAF21085 standard; DNA; 1324 BP
    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-2000; 2000WO-US008020.
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                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2001 (first entry)
Query Match
Best Local Similarity 100.8
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-679539/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; 88.
                                                                                                                                                                                                                                                                                                                                                    AAF21085;
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transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy/ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary pulmonary transplantation rejection, pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAP18434 to AAP21843 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                            the present invention
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Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

9 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG Gaps ö Length 1324; Indels ; Score 104; DB 3; ; Pred. No. 6.2e-25; 0; Mismatches 0; 100.0%; Local Similarity 100. 1es 104; Conservative Query Match ઠે 셤

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810

GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104 811 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 854 61 ઠે 셤

ABZ96779 standard; DNA; 1324 BP (first entry) 17-0CT-2003 ABZ96779; RESULT 8

Human nucleic acid sequence. antisense;

antinflammatory steroid, ubiquinone; antinflammatory; antiallergic; antianteners antianteners; cytostatic; gene therapy; antienes gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds. lung dysfunction; nasal airway dysfunction;

Homo sapiens.

WO200285308-A2

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Aguilar Pabalan J, Katz E, S; Sandrasagra A, Li Y, Sar Tang L, Miller S, Nyce JW,

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WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired or respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid ubiquinone

Disclosure; SEQ ID NO 12021; 872pp; English

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the

Pharmaceutical composition for treating asthma, has antisense oligonuclectide containing less percentage of adenosine, targeted to nucleic acids associated with lung airway or lung dysfunction, and

WPI; 2003-093058/08.

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initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nuclectides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antinflammatory steroid and ubiquinone. A composition of the invention has antinflammatory, antiallergic, antiasthmatic, hypotensive, insering a respiratory, lung or malignant disease or condition may have a reventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an inifialmmatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of adenosine receptor, producing bronchodilation, increasing bronchoconstriction, lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allegates, or a respiratory disease or condition. Note: The sequence date for this patent is not represented in the printed a special and a subject is not represented in the printed or specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pulmonary and inflammatory target DNA #239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. 6.2e-25; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 104;
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Matches 104; Conservative
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Human; antisense; bronchoconstriction; allergy; hyposecretion; pain; respiratory tract inflammation; adenosine sensitivity; lung; cancer; surfactant depletion; antiallaergic; antimflammatory; antiasthmatic; analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis; beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction; respiratory districtses syndrome; allergic rhinitis; pulmonary hypertension; emphysema; chronic obstructive pulmonary disease; cancer; bronchitis; pulmonary transplantation rejection; ds. Pabalan J, Aguilar D; Katz B, Li Y, Sandrasagra A, Ka Tang L, Shahabuddin S; 23-APR-2002; 2002WO-US013143. 24-APR-2001; 2001US-0286036P. (EPIG-) EPIGENESIS PHARM INC WO200285309-A2. Homo sapiens 31-OCT-2002. Miller S, Nyce JW, 

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1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                     A human TNF protein which is modified from the sequence shown in AAP80728, including naturally courring allelic variants is claimed. Also claimed are: recombinant DNA sequences encoding the protein (AAN80219) and control sequences for expression; a vector; a transformed host cell; a method of producing the protein by culturing the host cell; pharmaceutical compsn. of the protein and a carrier and a method of treating tumour burden with the compsn. The muteins are capable of the range of biological activities exhibited by native TNF but exhibit improved stability and ease of purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human, tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                                                                            Human tumour necrosis factor muteins - having comparable biological activity with improved stability and ease of purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tumour-associated antigenic target (TAT) cDNA sequence #631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 104; DB 1; Length 1560; Best Local Similarity 100.0%; Pred. No. 6.5e-25; Matches 104; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAATCTGGAGGCCACTTTGGTTCTGGCCAGAATGCTGC 104
                                                                                                                                                                                  Yamamoto R;
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1-1 to 1-2; 51pp; English.
                                                                                                                                                                                  Lin LS, Thomson JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ83817 standard; cDNA; 1581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2002; 2002US-0418988P.
                        88WO-US000183.
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                                                                           87US-00019221
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                                                                                                                                                                                                                                   1988-271165/38.
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                                                                                                                               (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                           P-PSDB; AAP80728
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ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004060270-A2
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                           25-JAN-1988;
                                                                           26-FEB-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                               Mark DF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                         This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung expression or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antialflammatory, antiathmatic, antiaged, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to composition and and and and and and associated inflammation, allergies and/or bronchoconstriction and session with a disease or condition set has pulmonary vessions or with a disease or condition are man are pulmonary vessions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic thinhitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to prevent any unwanted effects due to it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACACAGCTTTGATCCCTGACATCTG 810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 104; DB 11; Length 1324; Best Local Similarity 100.0%; Pred. No. 6.2e-25; Matches 104; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of pE4 encoding human tumour necrosis factor (TNF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           811 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 854
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                                                Claim 15; SEQ ID NO 12021; 763pp; English.
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86. .313
/*tag= a
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314. .787
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
bronchodilating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-DEC-1990
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C target (TAT) nucleic acid comprising; (a) any of 4622 nucleotide antigenic target (TAT) nucleic acid comprising; (a) the full-length coding region of a equences (see SEQ ID No:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) the full-length coding region of caquence identity to (a) - (c); or (e) a sequence that hybridises to (a) - (c) or (b); (d) a sequence that hybridises to (a) - (c) or (b); (d) a sequence that hybridises to (a) - (c) or the comprising the above expression vector; (3) a process for producing a polypeptide; (d) an isolated polypeptide (c) an amino acid sequence encoded by the full-comprising the above polypeptide; (d) an amino acid sequence encoded by the full-comprising the above polypeptide (used to a heterologous polypeptide; (c) an isolated antibody that binds to the above polypeptide; (f) a process (c) a sequence; (c) a sequence (c) a sequence; (c) a sequence (c) a protein antibody that binds to the above polypeptide; (f) a process (c) a sequence (c) a protein antibody; (g) a tinding organic molecule (in) a process (c) a producing the antibody; (g) an isolated oligopeptide; (f) a process (c) an isolated antibody that binds to the above polypeptide; (f) a tinding organic molecule that binds to the above polypeptide; (f) a tinding organic molecule that binds organic molecule, in combination with a carrier; (l1) an article of manufacture comprising the container; (12) methods of the composition of matter contained within the container; (12) methods of the proveh of the above protein; (l3) a method for treating a mammal having a cancerous tumour comprising cells that expresses the above protein; (l3) a method for treating an animal and containing the protein of greence of a protein an associated with increased expression or activity of the above protein; (l4) a method for treating an expression or activity of the above protein; and (l7) a method for treating an expression or activity of the above protein; the protein molecule to a cell that express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   999 GAATICAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reventing or treating cancer. The composition is also used for preparing medicament for the therapeutic treatment or diagnostic detection of a bil proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                         The present invention describes an isolated tumour-associated antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.
New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 104; DB 12; Length 1581;
100.0%; Pred. No. 6.5e-25;
cive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1581 BP; 351 A; 471 C; 385 G; 374 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1059 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAATCTGGAGCCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human TAT cDNA sequence from the present invention.
                                                                       Claim 1; SEQ ID NO 631; 5504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN60557 standard; DNA; 1585 BP
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preventing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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1003 GAATICAAACIGGGCCICCAGAACICACIGGGGCCIACAGCIIIGAICCCIGACAICIG 1062
                                                                                                                                                                                                                                                                                                                                                                 The sequence encoding TNF produced by the promyelocytic leukemia cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in B.coli (see AAN60557). Neither of the cysteine residues (69 and 101) in the TNF sequence appears to be involved in disulphide linkages. The patentors claim a novel synthetic mutein of a biologically active hTNF protein, awaying at least one cysteine residue free from a disulphide link and non-essential to the activity and having at least one of the cysteine residues deleted or replaced by another AA. Plasmid pAW711 (Ser 69) is
                                                                                                                                                                                                                                                                                               New synthetic muteins of human tumour necrosis factor protein - are obtd.
by direct mutagenesis and retain antitumour activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1063 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 104; DB 1;
Pred. No. 6.5e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human TNF-alpha DNA corresponding to M10988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                           Lu SDY, Wang AM;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 1, 47pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACA64836 standard; DNA; 1585 BP.
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                                                                                                                                         86WO-US000236
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                                                                                                                                                                     85US-00698939
                         /*tag= a
314 .787
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 104; Conservative
                                                                                                                                                                                                                                                      WPI; 1986-225458/34.
                                                                                                                                                                                               (CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                           Lin LS,
                                                                                                                                                                                                                                                                      P-PSDB; AAP60655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE10127572-A1
                                                                                                                                         03-FEB-1986;
                                                                                                                                                                   07-FEB-1985;
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                                                                                 WO8604606-A.
                                                                                                              14-AUG-1986.
                                         mat_peptide
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                                                                                                                                                                                                                          Mark DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claimed
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Key
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                                                                                                                                                                                                                                                                             definition and therapy of chronic inflammatory joint diseases, and other inflammatory diseases, and other inflammatory joint diseases, and other products of the invention have antinflammatory. Cytostatic, antiatchritic, antistheumatic and immunosuppressive activity and can be used for gene therapy. The reagent of the invention and any proteins and antibodies derived from it, are used (i) for analysing tissue and blood samples for medical diagnosis; (ii) for diagnosis and characterisation of chronic joint diseases, on the basis of molecular characterisation, and determining the etiological pathogenicity principle of as yet uncharacterised inflammatory diseases, also monitoring progression and/or treatment of disease, and optimisation of therapy and (iii) for developing treatments for inflammatory diseases, particularly of joints, infections and tumours. ACA64965 represent human polynucleotides used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                   Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; syrotoxic factor; cytotoxic factor; differentiation factor; nurspeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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                                                                                                                                                                                                                                                                    molecular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 104; DB 8; Length 1585; 100.0%; Pred. No. 6.5e-25; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted and transmembrane protein cDNA SegID 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1063 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106
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                                                                                                                                                                                                                                                                  This invention describes a novel reagent for diagnosis,
                                                                          Blaess S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF76346 standard; cDNA; 1585 BP
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30-MAY-2001; 2001DE-01027572.
                                                                                                                                                                                                                            Claim 1; Page; 12pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 104; Conservative
                                                                          Ungethuem U,
                                     (PATH-) PATHOARRAY GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                            WPI; 2003-240797/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                          Haeupl T,
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                                                                                                                                                                                       proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information.

The formation or differentiation is typically governed by information or eccived from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel provides the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is a cDNA sequence a human PRO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
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Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                     related disorder, e.g. systemic lupus erythematosus, rheumatoid
arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis
                                                                                                                  polypeptides, useful for diagnosing and treating an immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1585;
Schoenfeld JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1063 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteopathic; antiarthritic; antirheumatic; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 104; DB 10;
; Pred. No. 6.5e-25;
0; Mismatches 0;
Jackman JK,
                                                                                                                                                                                                               Claim 2; SEQ ID NO 19; 918pp; English.
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Hunte B,
, Wu TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI32003 standard; cDNA; 1585
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Matches 104; Conservative
                Wood WI,
  Clark H,
                                                       WPI; 2003-721702/68
                                                                                                                                                                              diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA #1329.
                                                                             P-PSDB; ADF76347
Bodary SC, C
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                  New PRO
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  셤
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Seilhamer JJ;
 98US-00023655.
                                                 Stuart SG,
                        (INCY-) INCYTE CORP.
09-FEB-1998;
                                                 Cocks BG,
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WPI; 2003-895307/82

A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.

Claim 1; SEQ ID NO 1329; 50pp; English.

The invention relates to a composition comprising a plurality of CDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comparising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detected the non-diseased sample, where an altered level of the detected hybridisation complexes and comparing the levels of the detected of hybridisation complexes or complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray for monitoring contextive colitis, hyperecosinophila, irritable bowel syndrome, culcerative colitis, hyperecosinophila, irritable bowel syndrome, contextifying agents for the treatment of the diseases. The microarray may also be used in furnation of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in purification of a subpopulation of may also be used in the printed specification but was obtained in electronic format directly format directly then the printed performance and a pure minimal partition. The presence of the discourse of the disc from USPTO at segdata.uspto.gov/sequence.html 

Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;

0; Gaps Query Match
100.0%; Score 104; DB 11; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0;

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Search completed: September 3, 2005, 00:29:34 Job time : 326.075 secs



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September 2, 2005, 23:36:03; Search time 2377.85 Seconds (without alignments) 1664.816 Million cell updates/sec
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104
1 gaattcaaactggggcctcc.....ggttctggccagaatgctgc 104
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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9b est2:

9b est4:

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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			عد			SUMMARIES	
Result No.	ult No.	Score	Query	Query Match Length DB	DB	ID	Description
!	-	104	100.0	474	5	BX118951	BX118951 BX118951
O	7	104	100.0	630	9	CB528492	٠
υ	М	104	100.0	645	9	CD370363	CD370363 UI-H-FT1-
υ	4	104	100.0	688	9	CD367676	CD367676 UI-H-FT1-
U	2	104	100.0	969	9	CA307225	CA307225 UI-H-FT1-
O	9	104	100.0	669	9	CD364761	CD364761 UI-H-FT2-
υ	7	104	100.0	703	9	CD368142	7
U	8	104	100.0	713	ဖ	CA308256	CA308256 UI-H-FT1-
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υ	10	104	100.0	722	S	BQ007008	BQ007008 UI-H-EI1-
O	11	104	100.0	722	9	CA307062	CA307062 UI-H-FT1-
υ	12	104	100.0	722	9	CD364988	CD364988 UI-H-FT2-
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U	15	104	100.0	724	9	CA309711	CA309711 UI-H-FT1-
ပ	16	104	100.0	726	9	CA310368	CA310368 UI-H-FT1-
υ	17	104	100.0	726	ø	CD368929	CD368929 UI-H-FT1-
υ	18	104	100.0	742	9	CA309509	CA309509 UI-H-FT1-
U	19	104	100.0	744	9	CD366187	CD366187 UI-H-FT1-
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υ	21	104	100.0	1068	н	AL543083	AL543083 AL543083
	22	103	0.66	248	7	T29839	T29839 EST97164 Hu
υ	23	103	99.0	693	9	CD367625	CD367625 UI-H-FT1-
U	24	102.4	98.5	684	9	CA307429	CA307429 UI-H-FT1-

CA309664 UI-H-FTI- CD367764 UI-H-FTI- CD240146 DTL3P2G5 AI24177 GH81908.x BG232086 naf32006.x CA748748 UI-H-FTI- AA597697 z178f12.8 AA59697 z178f12.8 AA69697 z178f12.8 AA69697 z178f12.8 AA69697 z178f12.8 AA69697 z178f12.8 AA69697 z178f12.8 AA69697 z178f12.8 AA69697 z178f12.8 AA69697 z178f12.8 CO33110 AGENCOURT BF407522 UI-R-BJ2- AL075400 DTC-GOBHI CE10980 t19r-GBB- CO049356 LG_mx0_11 CCA777347 964375 WA CA563031 K0308C04- BB840094 BB840094	BX118951 BX118951 BX118951 Scaree fetal heart NDHHJ9W Homo sapiens CDNA clone INAG959512143100 ; INAGE:1693595, mRNA sequence. INAG959512143100 ; INAGE:1693595, mRNA sequence. BX118951. GI:27882696 SET. NO BX118951. GI:27882696 SET. NO BX118951. GI:27882696 SET. SET. Homo sapiens (human) NISM Homo sapiens (human) NISM Homo sapiens (human) SERIATYORA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia Eutheria; Primates; Cararrhini; Hominidae; Homo.  AREA BEATL, L., Heil, O., Heminig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.  I Manual Uniquenced - RZPD3 NAL Unpublished (2009)  TR EZPD Deutsches Ressourcensentrum fuer Genomforschung GmbH RZPDIII I M.A. G. E. CDNA Clone Collection; Human Uniquenced - RZPD3 (Hosp) Sellibous-97 Contact: Ina Rolfs RZPD I McApp98112310.  RZPDIII J. M.A. G. G. CLON Clone Collection; Human Uniquenced - RZPD3 (Hosp) Sellibous-97 Contact: Ina Rolfs RZPD Deutsches Ressourcensentrum fuer Genomforschung GmbH RZPD Obettsches Ressourcensentrum fuer Genomforschung GmbH RZPD 10-10-10-10-10-10-10-10-10-10-10-10-10-1
CD309664 CD367794 CD367794 CD240146 AIZ42177 AIZ522086 CA748148 AIZ57811 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 AAC07062 CCC0049356 CCC0049356 CCC7777347	ALIGNMENTS  ALIGNMENTS  heart NbHH19  E:1693595, m  in ates; Cran  in ates; Cran  in ates; Cata  unig, S., Neub  D. and Korn,  D3 and Korn,  D3 and Korn,  D4 and Korn,  D5 and Korn,  D6 and Korn,  D7 and Korn,  D8 (RZPDLIB  neCards/Cgi-  pones? IbNo-  remaentrum f  Berlin, Germ  E e royalty-fr  pd.de) for f  pd.de) for f  ITTCACACAGG  ifiers  mo sapiens"  mno sapiens"  mno sapiens"  mno sapiens"  mno sapiens"  in and in and in and in and in and in and and and and and and and and and an
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4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BX118951 BX118951 BX118951 BX118951 BXCCESSION VERSION KEYWORDS SOURCE AUTHORE TITLE JOURNAL COMMENT FEATURES BOUIL
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ORIGIN

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/dev_stage="Adult"
/dev_stage="Adult"
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NCI_CGAP_FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 1-29, >AT rich#Low_complexity (matched compliment)
205-279, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
FOLYA=Yes:
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                          adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 124
double-stranded cDNA was size selected, ligated to Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 630) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      630 bp mRNA linear EST 05-AUG-
NCI_CGAP_FT2 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                     100.0%; Score 104; DB 5; Length 474; 100.0%; Pred. No. 2.7e-21;
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UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.
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/clone="UI-H-FT2-bjd-e-20-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                 Matches 104; Conservative
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CB528492/c
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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KEYWORDS
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construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 24 hours; RPA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Rtebsiella moi 10, 3 hours; Rtebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (AdS CWV eGFP), moi 500, 24 hours; Adenoviral vector (AdS CWV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; moi 500, 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours; wt adeno
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UI-H-FTI-bkb-n-03-0-UI.sl NCI CGAP_FTI Homo sapiens CDNA clone
UI-H-FTI-bkb-n-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONA DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CLONA DIStribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/Gapp.html
The following repetitive elements were found in this CDNA
sequence: 294-368, >(TAAA)n#Simple_repeat
DOLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          503 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 444
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/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP FT1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
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I (basea to 62 primates).
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG
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TAG TISSUE=Human Lung Alveolar Macrophage
TAG LIB=UI-H-FT2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Unpublished (1997)
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Matches 104;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              sequence: 69-143, > (TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                               Location/Qualifiers
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Matches 104; Conservative (
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Homo sapiens
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CA307225/c
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NCI CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different control 0. The macrophages in different control 10, a hours; RNA baurs; LPS 100 ng/ml, 3 hours; CAP hours; CAP hours; Rabbiella moi 10, 24 hours; Rabbiella moi 10, 3 hours; Staph aureus moi 10, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; At adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; At adenovirus moi 500, 3 hours; Ad vector + LPS 24 hours; Wt adenovirus + LPS 3 hours; Wt adenovirus + LPS 24 hours - The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, diggested with Not I, and cloned directionally into pT773-Pac vector. The oligonuclectide used to prime the synthesis of first-etrand cDNA contains a library age seminore that is located herwesn the Not I site.
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NCI_CGAP_FT1 Homo sapiens cDNA clone
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Editoric Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this CDNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 688)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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UI-H-FTI-bjr-1-14-0-UI 3', mRNA sequence.
CD367676
CD367676.1 GI:31151766
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TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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Homo sapiens
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CD367676/c
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/clone="U1-H-FTL-190"
//clone="U1-H-FTL-190"
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UI-H-FTI-bhu-n-04-0-UI.sl NCI CGAP FT1 Homo sapiens cDNA clone
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.
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TAG_LIB=UI-H-FT1
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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534 GAATCTGGAGGCGCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 491

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/(10) LOSGI-"NULLU (LITE TECHNOLOGIES)"
/(10) LOSGI-"NULLU (LITE TECHNOLOGIES)"
// Ince="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: BCOR 1; Site 2: Not 1;
// NOT CGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different construction. Control O hours; control 3 hours; Control on hours; control 3 hours; Rlebsiella moi 10, 24 hours; Rlebsiella moi 10, 24 hours; Raphsiella moi 10, 3 hours; Rlebsiella moi 10, 24 hours; Adenoviral vector (Ad5 CWV eCFP), moi 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector to 500, 24 hours; Ad vector to 500, 3 hours; Ad vector t
                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 696)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP ttp://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAG_TISSUE=Human Lung Alveolar Macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="Alveolar Macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |mol_type="mRNA"
|db_xref="taxon:9606"
|clone="UI-H-FT1-bhu-n-04-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
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Best Local Similarity 100.
Matches 104; Conservative
                              REFERENCE
AUTHORS
TITLE
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61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104

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/Gione="UJ-H-FT2-Dul"
//clone="UJ-H-FT2-Dul"
//dev eage="Adult"-11-0-UI"
//dev eage="Adult"-11-0-UI"
//dev beage="Adult"-11-0-UI"
//dev beage="Adult"-11-0-UI"
//deb host="DH10B (Life Technologies)"
//loce="Organ: Lung; Vector: pT7T3-pac (Pharmacia) with a modified polylinker; Site1: ECOR I; Site 2: Not I;
NOI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, The mRNA samples were booled for library construction. Control 0 hours; control 3 hours; control 24 hours; control 10 mg/ml, 3 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; control 10, 3 hours; LPS 100 ng/ml, 3 hours; Expl moi 10, 24 hours; Rebsiella moi 10, 3 hours; Staph aureus moi 10, 3 hours; wt adenovirus moi 500, 3 hours; wt adenovirus Hours; wt hunninghake of the University mon mon mand Soares; Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University
                                                                      CD364761
UI-H-FTZ-bjm-j-11-0-UI.81 NCI CGAP FTZ Homo sapiens CDNA clone
UI-H-FTZ-bjm-j-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencial printing to Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this CDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
BOUNA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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TAG_LIB=UI-H-FT2
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/db_xref="taxon:9606"
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Unpublished (1997)
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RESULT 6
CD364761/c
                                                                                                                   DEFINITION
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/tissue_type="Alveolar Macrophage"
/dev_etage="Alveolar Macrophage"
/dev_etage="Adult"
/lab host="DH10B (Life Technologies)"
/clone lib="NCI_CGAP_FTI"
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/note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: ECCR I; Site 2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, other donor macrophages in different conditions. The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 3 hours; control 3 hours; LPS 100 ng/ml, 4 hours; Ab hours; Klebsiella moi 10, 3 hours; Staph aureus moi 10, 24 hours; Abdenoviral vector (AdS CRV eGFP), moi 500, 24 hours; Ad enoviral moi 10, 3 hours; At adenovirus moi 500, 24 hours; At adenovirus Hours; Wt adenovirus + LPS 24 hours; Wt adenovirus + LPS 24 hours; Wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares Genome Research, 6:791-806, 1996. First strand cDNA synthesis was
                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 05-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Itsuse Procurement: Dr. dary W. Hunninghake, U of I

cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/cgap.html

The following repetitive elements were found in this cDNA

sequence: 298-372, >(TAAA) n#Simple_repeat
                                                                                                                                 1 GAATICAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 703) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                CD368142 703 bp mRNA linear EST 05-AUG-
UI-H-FT1-bjv-e-20-0-UI.81 NCI CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bjv-e-20-0-UI 3', mRNA sequence.
                                                 Gaps
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                                                                                                                                                                                                                                                      534 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 491
                                                                                                                                                                                                                    61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                              Indels
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            Pred. No. 2.9e-21;
100.0%; Pred. ....
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/mol_type="mRNA"
/db_xref="taxon:9606"
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CD368142.1 GI:31152232
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Unpublished (1997)
            Best Local Similarity 100.
Matches 104; Conservative
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TITLE
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COMMENT

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UUT-PFT1-bhye-14-0-UI"
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/clone="Lb="MCI_CGAP FTI"
/lab_host="DH10B (Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoslveolar lavage)
primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT) 18 tail. The sequence tag for this library is GGCATGCGT. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG IISSUE-Human Lung Alveolar Macrophage
TAG_LIB-UTH-FTI
TAG_SEQ-GGCCATGCCG"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soaresdulowa.edu
The following repetitive elements were found in this CDNA
Bequence: 296-370, > (TAAA) n#Simple_repeat
BOLYA=Yes.
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UI-H-FTI-bhy-e-14-0-UI.81 NCI_CGAP_FTI Homo sapiens cDNA clone
UI-H-FTI-bhy-e-14-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              596 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 713)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 104; DB 6; Best Local Similarity 100.0%; Pred. No. 2.9e-21; Matches 104; Conservative 0; Mismatches 0;
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/clone="UI-H-FT2-bjd-1-22-0-UI" /tissue\_type="Alveolar Macrophage"

type="mRNA" xref="taxon:9606"

us-09-801-371a-1.rst

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(some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Riebsiella moi 10, 3 hours; Riebsiella moi 10, 24 hours; Riebsiella moi 10, 3 hours; Riebsiella moi 10, 24 hours; Adenoviral vector (Ad5 CWV GGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CWV GGFP), moi 500, 24 hours; Ad hours; Adenoviral vector (Ad5 CWV GFP), moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; Wa adenovirus + LPS 3 hours; Wa adenovirus + LPS 24 hours; Wa propriet is a primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with not I, and cloned directionally into pT773-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that Is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunhinghake of the University of Iowa.

TAG_ILB=UI-H-FTI

TAG_ENGER
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/dev stage="Atvolar Macropinge"
//dev stage="Atvolar Macropinge"
//lab\_host="DH10B (Life Technologies)"
//clone llb="MCI (CGAP FT2:
//clone llb="MCI (CGAP FT2:
//note="Grgan: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site=1: EcoR I; Site\_2: Not I;
//clone llb="MCI (CGAP FT2: pT773-Pac (Pharmacia) with a modified polylinker; Site=1: EcoR I; Site\_2: Not I;
//note=Torparion is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, other donor macrophages in different conditions. The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Riebsiella moi 10, 3 hours; Adenoviral vector (AdS CNV eGFP), moi 500, 24 hours; Adenoviral vector (AdS CNV eGFP), moi 500, 24 hours; Adenoviral + LPS 3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 4 hours; when it is a subtracted according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University

ORIGIN

TAG\_TISSUE=Human Lung Alveolar Macrophage TAG\_LIB=UI-H-FT2

TAG SEQ=GGCCATGCCG"

ORIGIN

RESULT 9
CB528694
CB528694
CB528694
CB528694
CB528694
UI-H-FT2-bjd-1-22-0-UI.81 NCI CGAP FT2 Homo sapiens CDNA clone
DEFINITION UI-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.
ACCESSION CB528694.1 GI:29388630
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
CRGANISM Homo sapiens (human)
CRGANISM EDIA CATAINA SEQUENCE.

NATHORS Homo sapiens (human)
CRGANISM EDIA CATAINA SEQUENCE.

NATHORS Homo sapiens (human)
CRGANISM CASTAINA SEQUENCE.

NATIONAL CANEET LOAPE IN PRIMATES (CASATAINA); HOMINIDAS; HOMO.
TITLE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

CORRANIS NCI-CGAP http://www.ncbi.nlm.nih.gov
TITLE
TITLE
TUMOR Gane Index
JOURNAL
CONTACT: ROBERT STRUMBERG, Ph.D.
CONTACT STRUMBERG, PH.D.
CONTACT

Location/Qualifiers

source

FEATURES

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אראביליטס (אבריביטס ב-22 pp mRNA linear EST 26-MAR-2002 UI-H-EII-azb-j-22-0-UI.81 NCI CGAP_EII Homo sapiens cDNA clone IMAGE:5846517 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                       592 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 533
                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 722) NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                            1 GAATICAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
                                                   Gaps
                                                ö
100.0%; Score 104; DB 6; Length 719; 100.0%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                  532 GAATCTGGAGACCGGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 489
                                                                                                                                                                                       61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                              0; Indels
                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ007008.1 GI:19731908
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Unpublished (1997)
                                              Matches 104; Conservative
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Query Match
Best Local Similarity
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ORGANISM
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BQ007008/c
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/clone="IMAGE:5846517"
/tissue_type="Chondrosarcoma"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_EII"
/lote="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT) latil. The sequence tag for this library is
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
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UI-H-FTI-bhu-o-04-0-UI.81 NCI CGAP_FTI Homo sapiens CDNA clone
UI-F-FII-bhu-o-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   595 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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1 (Dases 1 to 722)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                through the I.M.A.G.B. Consortium/Linl. at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
Clone Distribution: Clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 104; DB 5; Length 722; 100.0%; Pred. No. 2.9e-21; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=chondrosarcoma
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_TISSUE=chondrosa
TAG_LIB=UI-H-EI1
TAG_SEQ=ACACTTGCAC"
                                                                                                                                                                                          Location/Qualifiers
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CA307062.1 GI:24470116
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Homo sapiens
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Matches 104; Conserv
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유 ò 유

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/docume="UI-Haxon:bub"
/(docume="UI-Haxon:bub"
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/(docume="UI-Haxon:bub"
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/(doc
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UI-H-FT2-bjn-c-04-0-UI.81 NCI CGAP_FT2 Homo sapiens cDNA clone
UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.
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The following repetitive elements were found in this cDNA equence: 295-369, > (TAAA)n#Simple_repeat
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TAG LIB-UI-H-FT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 490
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                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                          Location/Qualifiers
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                                    sequence: 295-369, > (TAA
Seg primer: M13 FORWARD
POLYA=Yes.
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="Ul-HrPT2-Duc-14-0-Ul"
/tissue_type="Alveolar Macrophage"
/dev_etage="Adute"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FT2"

                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONA DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CLONA Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/Gagp.html
The following repetitive elements were found in this CDNA
sequence: 297-371, *(TAAA)n#Simple_repeat
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Euteria, Primates; Catarrhini, Hominidae, Homo. 1 (Dases 1 to 722)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-OGAP Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels
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TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                   REFERENCE
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RESULT 13 CA308777/c

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ULH-FTI-bhy-b-23-0-UI 3', mREM sequence.

OA308777.1 G1:24471831

EST.

CA308777.1 G1:24471831

EST.

EST.

Home sepiens (human)

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RESULT 15
CA309711/c
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TITLE
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/dev_stage="Adult"
/dev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          were a mixture of these countions (times ferein to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, other donor macrophages in different conditions, other donor macrophages in different conditions. The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; control 10 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; Rlebsiella moi 10, 3 hours; Rlebsiella moi 10, 3 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; wt adenovirus soi 500, 3 hours; wt adenovirus + LPS 4 hours; The library was normalized according to Bonaldo, Lennon and Soares, Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD368116 1723 bp mRNA linear EST 05-AUG-2004 UI-H-FT1-bjv-a-04-0-UI.81 NCI CGAP FT1 Homo sapiens cDNA clone UI-H-FT1-bjv-a-04-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this CDNA
sequence: 297.371, > (TAAA) n#Simple_repeat
                                                                                                                                                                                                                                                                      595 GAATICAAACIGGGGCCTCCAGAACICACIGGGGCCTACAGCITIGAICCCTGACAICIG 536
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 723)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                              Gapa
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                       Length 723;
                                                                                                                                                                                                                                                                                                                                                             61 GAATCTGGAGACCAGGGCCTTTGGTTCTGGCCAGAATGCTGC 104
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                                                                                                     Indels
    100.0%; Score 104; DB 6;
100.0%; Pred. No. 2.9e-21;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Query Match
Best Local Similarity 100.
Matches 104; Conservative
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AUTHORS
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KEYWORDS
SOURCE
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Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_IISSUE-Human Lung Alveolar Macrophage
TAG_LIB-UI-H-FT1
TAG_SEQ=GGCCATGCCG"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this CDNA
sequence: 297-371, > (TNAA) n#Simple_repeat
PODYA-Yes.
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/dev_stage="Adult"
/dev_stage="Adult"
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
CCGAP FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA309711 724 bp mRNA linear EST 05-AUG-2004 UI-H-FT1-bic-b-17-0-UI.sl NCI CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bic-b-17-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 104; DB 6; Length 723; 100.0%; Pred. No. 2.9e-21; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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/organism="Homo sapiens"
/mol_type="mRNM"
/db_xref="taxon:9606"
/clone="UI-H-FT1-bic-b-17-0-UI"
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Tue Sep

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incubations following isolation by bronchoalveolar lavage)

(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; LAS long ng/ml, 24 hours;
PMA 10 ng/ml, 3 hours; LPA 10 ng/ml, 24 hours; Klebsiella
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Rebsiella
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (AdS CMV eGFP), moi 500, 24 hours; Adenoviral vector
(AdS CMV eGFP), moi 500, 24 hours; Ad vector + LPS
3 hours; Ad vector + LPS 24 hours; The library was
normalized according to Bonaldo, Lennon and Soares Genome
Research, 6:791-806, 1996. First strand cDNA synthesis was
primed with no oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an ECOR I adaptor,
digested with Not I, and cloned directionally into
pT73-Pac vector. The oligomucleotide used to prime the
synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(4T) 18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
TAG_LIB-UI.+FTI
TAG_ESEQ=GGCCATGCCG."
```

Query Match
100.0%; Score 104; DB 6; Length 724;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps

ORIGIN

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Search completed: September 3, 2005, 02:11:40 Job time: 2384.85 secs

Sequence 11804, A Sequence 15358, A Sequence 15735, A Sequence 14033, A Sequence 12777, A Sequence 12147, A Sequence 12147, A Sequence 13187, A Sequence 13187, A Sequence 17361, A Sequence 15, Appl Sequence 15, Appl Sequence 13, Appli Sequence 13, Appli

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Score 104; DB 4; Length 787; Pred. No. 4.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEB Bochringer Ingelheim Corporation STRET: 900 Ridgebury Road, P.O. Box 368
CITY: Ridgefield
STATE: Connecticut
COUNTRY: United States of America
ZIP: 06877-0368
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: NEW PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,297A
FILING DATE: 27-FED-1998
CLASSIFICATION NUMBER: 06/038,266
FILING DATE: 28-FEB-97
ATTORNEY/AGENT INFORMATION:
NAME: ROBERT NUMBER: 25089
REFERENCE/DOCKET NUMBER: 9/121PCT
TELECOMMUNICATION NUMBER: 9/121PCT
TELECOMMUNICATION NUMBER: 9/121PCT
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Revati J. Tatake, Steven D. Marlin and
Randall W. Barton
           US-09-949-016-11804
US-09-949-016-15358
US-09-949-016-15358
US-09-949-016-16773
US-09-949-016-16773
US-09-949-016-12177
US-09-949-016-12177
US-09-949-016-12147
US-09-949-016-12147
US-09-270-767-29222
US-09-270-767-29222
US-09-169-768-13
US-09-169-768-13
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US-09-169-768-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: TNFa 3' untranslated region SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09032297A Patent No. 6525184 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 203-791-6183
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: DNA
                                      26.0 2903
26.0 12695
26.0 8284019
25.6 22287
25.6 767677
25.4 188
25.4 3171
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                  US-09-032-297A-13
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                                                                                                     1, Appli
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16898, A
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13517, A
13518, A
165185,
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16396, A
19072, A
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                                                                                                 2, 2005, 13:14:57; Search time 424.49 Seconds (without alignments) 400.888 Million cell updates/sec
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                                                                                                                                                                                             1 gaattcaaactggggcctcc......ggttctggccagaatgctgc 104
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-032-297A-13

US-09-229-151C-7

US-09-229-151C-7

US-09-949-016-5156

US-09-505-520-4

US-09-229-151C-14

US-09-166-1186-1

US-09-166-1186-1

US-09-166-1186-1

US-09-106-11898

US-09-949-016-16898

US-09-949-016-16898

US-09-949-016-16806

US-09-949-016-16806

US-09-949-016-15603

US-09-949-016-13517

US-09-949-016-13517

US-09-949-016-13518

US-09-949-016-13518

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US-09-949-016-13518
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                                                                                                                                                                                                                                                                      1202784 segs, 818138359 residues
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                                                                                                                                                                                                                                                                                                                                                                            Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     nucleic search, using sw model
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seq length: 200000000
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10728
                         Copyright
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32.6 29.2 29.2 29.2

10001 10001 10001 10001 10001 10001 10001

Result

28.4 28 28 28

227.8 227.8 227.8 4.7.7 2.7.4 3.7.4

Post-processing:

Database

Minimum DB Maximum DB

Scoring table:

Searched:

Perfect score:

Sequence:

OM nucleic

Run on:

us-09-801-371a-1.rni

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GENERAL INFORMATION:

APPLICAMT: VENTER, J. Craig et al.

APPLICAMT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSESEQ FOR Windows Version 4.0

LENGTH: 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1005 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 104; DB 4; Length 1585; 100.0%; Pred. No. 5.4e-27; ive 0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%; Pred. No. 5.4«
Matches 104; Conservative 0; Mismatches
                                                                                     FILING DATE:
CLASSIFICATION:
ATTORNEY, AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTAATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
TELECHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEC ID NO: 1329:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 5156, Application US/09949016; Patent No. 6812339
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Best Local Similarity 100.0
Matches 104; Conservative
  FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    STREAM TOPOLOGY: 11near IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5156
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APPLICANT: Tatake, Revati J.

APPLICANT: Marin, Steven D.

APPLICANT: Marin, Steven D.

APPLICANT: Marin, Steven D.

TITLE OF INVENTION: Salf-Regulated Apoptosis of Inflammatory Cells by Gene Therapy

FILE REFERENCE: 9/137

CURRENT FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: US 60/076,316

PRIOR FILING DATE: 1999-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 281
                                                                                            222 GAATICAAACIGGGGCCICCAGAACICACIGGGGCCIACAGCIITGAICCCTGACAICIG 281
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Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Ocffrey J. Sallhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
  Gaps
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100.0%; Pred. No. 4.2e-27;
Live 0; Mismatches 0; Indels (
                                                                                                                                                                        282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 325
                                                                                                                                            61 GAATCTGGAGCCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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0; Indels
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COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: TNF-alpha untranslated region US-09-229-151C-7
  0; Mismatches
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APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09229151C
Patent No. 6537784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 15
SOFWARE: Patentin version 2.0
SEQ ID NO TENGTH: 787
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Matches 104; Conservative
  Matches 104; Conservative
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MEDIUM TYPE: Floppy
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ORGANISM: Human
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                                                                                                                                                                                                                                                                  RESULT 2
US-09-229-151C-7
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; FEATURE;
NAME/KEY: CDS
; LOCATION: (153)...(854)
US-09-505-250-4
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ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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US-09-505-250-4
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                                                                                                       APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Laderoute, Keith R.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
TUTNER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-UN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/1B95/00996
FILING DATE: 13-NOV-1995
FILING DATE: 13-NOV-1995
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/365,486
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: SADILZ, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 38,615
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELECOMMUNICATION FOR SEQ ID NO: 36:
SEQUENCE: CHARACTERISTICS:
TENENTH: 1643 base pairs
TYPE: mucleic acid
STRANDEDNESS: double
TYPE: MUCLEIC ACID
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                                                                                                                                                                                                                                                                            STREET: Deblinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                   Sequence 36, Application US/08880342
Patent No. 6218179
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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US-08-880-342-36
               US-08-880-342-36
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GENERAL INFORMATION:
APPLICANT: Tatake, Revati J.
APPLICANT: Tatake, Revati J.
APPLICANT: Maxlin, Steven D.
APPLICANT: Barton, Randall W.
TITLE OF INVENTION Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy FILE REPREBACE: 9/131C
CURRENT APPLICATION NUMBER: US/09/229,151C
CURRENT PILING DATE: 1999-01-12
PRIOR PILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 2.0
SEQ ID NO 13
LENGTH: 2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1643;
Sequence 4, Application US/09505250A

Sequence 4, Application US/09505250A

Patent No. 6329148

GENERAL INFORMATION:
APPLICANT: Rosen, Glenn
APPLICANT: Kao, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: Triptolides and Death Domain Ligands
FILE REFERENCE: SUN-109PRV2
CURRENT APPLICATION NUMBER: US/09/505,250A

CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1130 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 1173
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US-09-229-151C-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 104; DB 3; Best Local Similarity 100.0%; Pred. No. 5.5e-27; Matches 104; Conservative 0; Mismatches 0;
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; Sequence 13, Application US/09229151C
; Patent No. 6537784
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2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867
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; Sequence 1, Application US/09313932A
; Sequence 1, Application US/09313932A
; GENERAL INFORMATION:
    APPLICANT: Baker, Brenda
; APPLICANT: Bannett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Butler, Madeline M.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE MODULATION OF TNF-
; TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE MODULATION OF TNF-
; TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE MODULATION OF TNF-
; TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
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LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
                                                                                                                                                NATE/CATION: (2171)..(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Saidguchi, A.Y.
AUTHORS: Smith, D.
AUTHORS: Jarrett.Nedwin, J.
AUTHORS: Gray, P.W.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factifies homology and chromosomal localization JOURNAL: Nucleic Acids Res.
VOLUME: 13
ISSUE: 17
ISSUE: 17
ISSUE: 17
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DATABASE ACCESSION NUMBER: X02910 Genbank

J DATABASE ENTRY DATE: 1997-02-17

DATABASE TURKY DATE: 1997-02-17
                         FEATURE:
NAME/KEY: intron
LOCATION: (1870)..(2070)
LOCATION: (1822)..(1869)
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LOCATION: (982)..(1588)
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ORGANISM: Homo sapiens
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LOCATION: (615)..(981)
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LOCATION: (1589).
FEATURE:
NAME/KEY: intron
                                                                                                                                  NAME/KEY: exon
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                                                    Sequence 144, Application US/09229151C

Batent No. 6537784

GENERAL INFORMATION:

APPLICANT: Barton, Randall W.

APPLICANT: Barton, Randall W.

TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy

FILE REFERENCE: 9/137

CURRENT APPLICATION NUMBER: US/09/229,151C

CURRENT APPLICATION NUMBER: US/09/229,151C

PRIOR APPLICATION NUMBER: US 60/076,316

SOFTWARE PARENT APPLICATION NUMBER: US 60/076,316

BRIOR APPLICATION NUMBER: US 60/076,316

BRIOR APPLICATION NUMBER: US 60/076,316

CHRENT APPLICATION NUMBER: US 60/076,316

CHRENT APPLICATION NUMBER: US 60/076,316
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Sequence 1, Application US/09166186A

Patent No. 6080580

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Benetr, C. Frank

APPLICANT: Butler, Madeline M.

APPLICANT: Butler, Madeline M.

APPLICANT: Shanahan, William R.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION FILE REFERENCE: ISPH-0322

CURRENT APPLICATION NUMBER: US/09/166,186A

CURRENT FILING DATE: 1998-10-05

NUMBER OF SEQ ID NOS: 250

SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2065 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2108
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NAME/KEY: CDS
TEATURE:
NAME/KEY: CDS
FEATURE:
NAME/KEY: exon
LOCATION: (615)..(981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR
US-09-229-151C-14
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NAME/KEY: exon
LOCATION: (1589)..(1634)
FEATURE:
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LOCATION: (1635)..(1821)
FEATURE:
NAME/KEY: exon
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LOCATION: (982)..(1588)
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ORGANISM: Homo sapiens
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ORGANISM: Human
FEATURE:
                                               US-09-229-151C-14
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2808 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 2867
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100.0%; Pred. No. 1.1e-26;
tive 0; Mismatches 0;
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; OTHER INFORMATION: recombinant vector pDATH-TNF?
US-09-376-774-5
                                                                                                                                          US-09-949-016-16898
; Sequence 16898, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 100.(
Matches 104; Conservative
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ORGANISM: Unknown
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Patent No. 6277981

GENERAL INFORMATION:

APPLICANT: Tw. Guang-Chou

APPLICANT: Israel, Yedy

TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF

TITLE OF INVENTION: EPPICACIOUS ANTISENSE OLIGONUCLEOTIDES

FILE REFERENCE: 9855-3U1

CURRENT APPLICATION NUMBER: US/09/109,663

CURRENT FILING DATE: 1998-07-03

BARLIER FILING DATE: 1997-07-03

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 34
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                                                                                                                                2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911
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100.0%; Score 104; DB 3;
Best Local Similarity 100.0%; Pred. No. 7.3e-27;
Matches 104; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34
                                                                 FEATURE:
NAME/KEY: intron
LOCATION: (1870)..(2070)
LOCATION: (1635)..(1821)
                                 NAME/KEY: exon
LOCATION: (1822)..(1869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                         FEATURE:
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FACENT NO. 'GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/29/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-03

PRIOR FILING DATE: 2000-00-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
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US-09-376-774-5/c
; Sequence 5, Application US/09376774
; Patent No. 675236
; GENERAL INFORMATION:
; APPLICANT: Fung, Yuen Kai
; APPLICANT: Fung, Yuen Kai
; TTILE OF INVENTION: Methods To Enhance And Confine Expression
; TTILE OF INVENTION: Methods To Enhance And Confine Expression
; TTILE OF INVENTION: Of Genes
; FILE REFERENCE: D6087
; CURRENT PILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/096,947
; FILE REPERENCE: 1998-08-18
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 5
; LENGTH: 10728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 104; DB 4; Length 6682; Best Local Similarity 100.0%; Pred. No. 9e-27; Matches 104; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4159 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 4202
                                                           2868 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 2911
61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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Search completed: September 2, 2005, 18:55:18 Job time : 428.49 secs
US-09-949-016-182065
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US-09-976-594-142/c

I Sequence 142 Application US/09976594

FREEDER 142 Application US/09976594

FREEDER 142 Application US/09976594

GENERAL INFORMATION:

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT PILING DATE: 2001-10-12

PRIOR FILING DATE: 2001-10-12

PRIOR FILING DATE: 2000-10-12

PRIOR FILING DATE: 2000-10-12

SOFTWARE: PERL PROGRAM

SOFTWARE: PERL PROGRAM

LENGTH: 2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 182065, Application US/09949016
Fatent No. 6812339
GENERAL INFORMATION:
FAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01307
CURRENT PELICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 182065
LENGTH: 601
TTYPE: DNA
ORGANISM: Human
                                             4220 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 4161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.3%; Score 32.6; DB 4; Length 2623; 58.9%; Pred. No. 0.14; Live 0; Mismatches 39; Indels 0;
                                                                                                                                      4160 GAATCTGGAGACCAGGAGCCTTTGGTTCTGGCCAGAATGCTGC 4117
                                                                                                         61 GAATCTGGAGACCAGGGGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

CTHER INFORMATION: Incyte ID No. 6673549 337187.1

NAME/KEY: unsure

LOCATION: 2612

CTHER INFORMATION: a, t, c, g, or other

US-09-976-594-142
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Matches 56; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-09-949-016-182065
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355 CAGACTGTGCCACGCAGAGCTCCTGGGGGCTTTTTTTTTCACCTCAGATATTTTGAAAC 414
                                                                                   6 CAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTGGAATC
                                           Gaps
                                           ;
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  Score 29.2; DB 4; Length 601;
Pred. No. 1.4;
0; Mismatches 23; Indels
    28.1%;
Query Match
Best Local Similarity 65.2<sup>3</sup>
Matches 43; Conservative
                                                                                                                                                                                                      415 TGAAGA 420
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1901, Ap 1901, Ap 6, Appli 1, Appli 6, Appli

Appli Appli

Sequence 4 Sequence 9 Sequence 1

Sequence

Sequence

43

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APPLICANT: Kaempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
I APPLICANT: Bulled ABOULLY, YIZZHAK
ITILE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
ITILE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR PILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ FOR Windows Version 4.0
18 US-10-641-643-1329
18 US-10-715B-19
18 US-10-72-411-4
18 US-10-72-411-4
18 US-10-72-411-4
18 US-10-72-411-9
19 US-10-72-9
19 US-10-72-9
10 US-10-72-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-801-371A-8
US-09-801-371A-2
US-09-801-371A-6
US-09-796-692-6223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/09801371A; Patent No. US20020155569A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
     Sequence 13, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 501, App
Sequence 501, App
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Sequence 5, Appli
                                                                                                                                                                     7; Search time 478.966 Seconds (without alignments) 1421.994 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                       1 gaattcaaactggggcctcc......ggttctggccagaatgctgc 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                         5.1.6
Compugen Ltd
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US-10-895-393-9
US-10-814-634A-5
US-10-172-118-501
US-10-342-887-501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                            7338684 segs, 3274456166 residues
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US-09-801-371A-5
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                         GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                     September 2, 2005, 15:27:57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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length: 2000000000
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104
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Length 104; 0; Indels 1 GAATICAAACIGGGGCCTCCAGAACICACIGGGGCCTACAGCTTTGAICCCTGACAICTG 

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Result

Sequence 6, Appli Sequence 1, Appli Sequence 17, Appli Sequence 17, Appl Sequence 17, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli Sequence 1, Appli Sequence 18012, A Sequence 18012, A Sequence 18012, A Sequence 120, Appli Sequence 120, Appli Sequence 120, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

Beq Beq

Minimum DB Maximum DB

Database :

Title: Perfect score:

Seguence:

OM nucleic

Run on:

Scoring table:

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Sequence 9, Application US/10895393

Sequence 9, Application US/10895393

Publication No. US20050048549A1

GENERAL INFORMATION:
APPLICANT: CAO, Liangxian

APPLICANT: MEHTA, Anuradha

APPLICANT: MEHTA, Anuradha

APPLICANT: FRIFILLIS, Panayiota

APPLICANT: TRIFILLIS, Panayiota

APPLICANT: TROTTA, Christopher R.

TITLE OF INVENTION: Methods and Agents for Screening for Compounds Capable of Modulat

TITLE OF INVENTION: Expression

FILE REFERENCE: 19025.012

CURRENT APPLICATION NUMBER: PCT/US04/01643

FRIOR TLING DATE: 2004-07-21

FRIOR APPLICATION NUMBER: PCT/US04/01643

FRIOR PILING DATE: 2003-01-21

FRIOR PELING DATE: 2003-01-21

WUMBER OF SEQ ID NOS: 24

SOFTWARKE PATENTION NUMBER: A0/441,637

FRIOR FILING DATE: 2003-01-21

NUMBER OF SEQ ID NOS: 24

SOFTWARKE: PatentIn version 3.1

SEQ ID NO 9

LENGTH: 798

FRIOR PATENTION NUMBER: A0/441,637

FRIOR PATENTION NUMBER: A0/441,637

FRIOR PAPILICATION NUMBER: A0/441,637

FRIOR PAPILICATION NUMBER: A0/441,637

FRIOR APPLICATION NUMBER: A0/441,637

FRIOR APPLICATION NUMBER: A0/441,637

FRIOR PAPILICATION NUMBER: A0/441,637

FRIOR APPLICATION NUMBER: A0/441,637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                          61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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APPLICANT: Novation Pharmaceuticals Inc.
TITLE OF INVENTION: Assay for Identifying Compounds Which
TITLE OF INVENTION: Affect Stability of mRNA
FILE REFERENCE: 793-104CIP
CURRENT APPLICATION NUMBER: US/10/814,634A
                                                                                                               100.0%; Score 104; DB 18;
100.0%; Pred. No. 7.2e-28;
iive 0; Mismatches 0;
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100.0%; Pred. No. 7.2e-28;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 104; Conservative
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                              Best Local Similarity
Matches 104; Conserv
   PAGES: 6361-6373
                           DATE: 1985
US-10-356-308A-13
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US-10-814-634A-5
                                                                                                                     Query Match
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| Sequence 13, Application US/10356308A
| Publication No. US20040039186A1
| GENERAL INFORMATION:
| APPLICANT: Martin, Steven D.
| APPLICANTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy |
| FILE REFERENCE: 9/121-1-CIP]
| CURRENT FILING DATE: 2003-01-31
| PRIOR APPLICATION NUMBER: US 69/032,297
| PRIOR APPLICATION NUMBER: US 60/039,266
| PRIOR FILING DATE: 1997-02-28
| NUMBER OF SEQ ID NOS: 13
| SEQ ID NO 13
| SEQ ID NO 13
| LENGTH: DATE: Patentin version 3.0
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1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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APPLICANT: Osman, Fariat
APPLICANT: Barzous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPUDLATION OF WENA SPLICING AND ITS USES
FILE REFERENCE: A34064-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
PRIOR TELLIG DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 2001-03-07
PRIOR PLING DATE: 1999-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 104;
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                                                       61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
                                                                                                               61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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ORGANISM: Homo sapiens
FEATURE:
LOCATION: 1 to 787
OTHER INFORMATION: TNFa 3' untranslated region
PUBLICATION INFORMATION:
PUBLICATION INFORMATION:
JOURNAL: Nacleic Acid Research
VOLUME: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 104; DB 9;
100.0%; Pred. No. 5.2e-28;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 12
SOFTWARES FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 104
                                                                                                                                                                                                                                                                Sequence 5, Application US/09801371A
Patent No. US20020155569A1
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5
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US-09-801-371A-5/c
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                     227 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Van t Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
PRIOR APPLICATION NUMBER: 06/380,770
PRIOR FILING DATE: 2002-05-14
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                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 104; DB 20; Best Local Similarity 100.0%; Pred. No. 7.2e-28; Matches 104; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: US 09/869,159
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: GB 9828709.7
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASESEQ for Windows Vergion 4.0
SEQ ID NO 5:
LENGTH: 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 501, Application US/10172118
Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Roberts, Chris
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DATABASE ACCESSION NUMBER: NM 000594
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501
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; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENRRAL INFORMATION:
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Best Local Similarity 100.0
Matches 104; Conservative
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                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
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LENGTH: 1585
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APPLICANT:
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1003 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACAGACTGTG 1062
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                                                            APPLICANT: Noberts, Christopher J.
APPLICANT: Noberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 3301-88-99
CURRENT APPLICATION NUMBER: 60/298,918
FRIOR FILING DATE: 2003-01-15
FRIOR FILING DATE: 2003-05-14
FRIOR APPLICATION NUMBER: 60/380,710
FRIOR FILING DATE: 2002-05-14
FRIOR PRILOG DATE: 2002-05-14
FRIOR FILING DATE: 2002-06-14
FRIOR FILING DATE: 2002-06-14
FRIOR SEQ ID NOS: 2699
SEQ ID NO 501
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; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Jeffrey J. Seilhamer
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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100.0%; Pred. No. 8e-28;
tive 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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NAME: Zeller, Karen J.
REGISTRAATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
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FILING DATE: 14-Aug-2003
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: <Unknown>
                                              Mao, Mao
Roberts, Christopher J.
Van 't Veer, Laura Johanna
Van de Vijver, Marc J.
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He, Yudong
Linsley, Peter S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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Best Local Similarity 100.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-10-342-887-501
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ORGANISM: human
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Publication No. US20040258678A1
GENERAL INFORMATION:
Patin Docket Preview
Patin Docket Preview
Patin Docket Preview
Patin Docket Preview
Patin CANT: BODARY, SARAH C.
APPLICANT: BRISDELL, HUNTE
APPLICANT: JACKAN, JANET
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WO, THOMAS. P. MICKEY
APPLICANT: WO, THOMAS. I.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
                                                                                                                                                                                                                                                                                                                                                                                         1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG
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100.0%; Score 104; DB 18; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 : US-10-641-643-1329
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CURRENT APPLICATION NUMBER: US/10/370,7159
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
LENGTH: 1585
Sequence 4, Application US/10272411
Publication No. US20030100068A1
GENERAL INFORMATION:
APPLICANT: Barnes Jewish Hospital
APPLICANT: Lam, Jonathan
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US-10-370-715B-19
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Sequence 3, Application US/10218547

Sequence 3, Application US/10218547

Publication No. US20030100074A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relative De INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relative De INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Relative De INVENTION: Mumber: US/10/218,547

CURRENT APPLICATION NUMBER: 60/312,542

PRIOR PILING DATE: 2001-08-16

PRIOR FILING DATE: 2001-0-10-30

NUMBER OF SEQ ID NOS: 57

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APPLICANT: ROSS, F. Patrick
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MINICS AND USES THEREOF
FILE REFERENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
CURRENT FILING DATE: 2002-10-15
PRIOR PILLING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
PUBLICATION INFORMATION
DATABASE ACCESSION NUMBER: NCBI/ X01394.1
DATABASE ENTRY DATE: 1995-03-21
KRIEVAMY RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-05-01
KRIEVAMY RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-05-01
KRIEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
KRIEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ M35592.1

RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-08-01
KRIEVAMY RESIDUES: (1)..(1643)
US-10-272-411-4
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1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129
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APPLICANT: Dai, Hongyue
APPLICANT: Linaley, Peter
APPLICANT: Linaley, Peter
APPLICANT: Linaley, Peter
APPLICANT: Mac, Mac, Mac, Mac, Mac, Marc, 
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PRIOR APPLICATION NUMBER: 60/180,908
PRIOR FILING DATE: 2000-02-08
PRIOR PILING DATE: 1909-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 71
SOFTWARE: Patentin version 3.12
SEQ ID NO 9
LENGTH: 1643
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Pred. No. 8.1e-28;
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DATABASE ENTRY DATE: 2001-06-18
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Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: human
US-10-310-793-9
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US-10-342-887-1901
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Best Local
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| Sequence 9, Application US/10310793|
| Publication No. US20030198640A1
| Sequence 9, Application Sequence 9, Application No. US20030198640A1
| Sequence 9, Application No. US20030198640A1
| Septicant: Vi, Guo-Liang APPLICANT: Vi, Guo-Liang APPLICANT: Ni, Jian APPLICANT: Ni, Jian APPLICANT: Ni, Jian APPLICANT: Resen, Pana APPLICANT: Wei, Ping TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta TITLE OF INVENTION: NUMBER: US/10/310,793
| CURRENT APPLICANTON NUMBER: US/26,294
| PRIOR PELLING DATE: 2001-12-07
| PRIOR PELLING DATE: 2001-08-24
| PRIOR PELLING DATE: 2001-08-24
| PRIOR PELLING DATE: 2001-08-24
| PRIOR PELLING DATE: 2001-07-06
| PRIOR FILING DATE: 2001-07-06
| PRIOR APPLICATION NUMBER: 06/216,879
| PRIOR APPLICATION NUMBER: 06/216,879
| PRIOR FILING DATE: 2000-07-07
| PRIOR APPLICATION NUMBER: 06/559,290
| PRIOR FILING DATE: 2000-07-07
| PRIOR APPLICATION NUMBER: 06/559,290
       1070 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 1129
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                                                                                                                  61 GAATCTGGAGACCAGGGAGCCTTTGGTTCTGGCCAGAATGCTGC 104
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Publication No. US2003010944A1

GENERAL INFORMATION:

APPLICANT: Barnes Jewish Hospital

APPLICANT: Lam, Jonathan

APPLICANT: Teitelbaum, Steven

TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF

FILE REFERENCE: 60019620-0206

CURRENT APPLICATION NUMBER: 05/20,10/272,328A

CURRENT APPLICATION NUMBER: 60/329,393

PRIOR APPLICATION NUMBER: 60/329,393

PRIOR APPLICATION NUMBER: 60/329,393

FRIOR PLING DATE: 2001-10-15

NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn version 3.1
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Pred. No. 8.1e-28;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 4
LENGTH: 1643
                                                                                                                                                                                                                                                                                       RESULT 12
US-10-272-328A-4
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US-10-310-793-9
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Search completed: September 3, 2005, 00:21:56 Job time : 484.966 secs

107541 Sequence 22
AR146199 Sequence
X01394 Human mRNA
BC020148 Home sapi
BD137687 Self-regu
AR300459 Sequence
BD137688 Self-regu
AR300460 Sequence
AR100270 Sequence
AR102270 Sequence
AR102270 Sequence
AR102270 Sequence
AR10227198 Antisense
BD277232 Predictio
BD66008 Novel exp
X0210 Human gene
AY066019 Homo sapi
AR10955 Sequence
AX100956 Sequence
AX100956 Sequence
AX100950 Sequence

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400 bp DNA linear STS 30-MAR-2000 SHGC-11076 Human Homo sapiens STS genomic, sequence tagged site. G13533.1 G1:1129272 STS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 400)

Olivier, M. and Cox, D.R.
Unpublished, Olivier, M., Cox, D.R. (2000)

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial incubation: 94 degrees C for 90 seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degrees C for 15
degrees C for 23
degrees C for 30
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62 degrees C for 2:
72 degrees C for 3(
30
Perkin Elmer 9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Michael Olivier, David R. Cox
Stanford Human Genome Center
Stanford University School of Medicine
4005 Miranda Ave. 2nd Fl., Palo Alto, CA 940
Faz: (650) 320-5800
Faz: (650) 320-5800
Fazi: (650) 320-5800
Fazi: 010vier@ehgc.stanford.edu
Primer A: CACTAAGATTCAAACTGGGGC
Primer B: GAGGAAGGCCTAAGGTCCAC
Firer B: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 ng
each 1 uM
each 200 uM
: 0.05 units/ul
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                                   AR146199
AR366225
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BD137687
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BDD217222
BDD64008
HSTNFA
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AB088112
AX100950
AX100965
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Annealing:
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Thermal Cycler:
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                        Primer:
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Protocol
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 DEFINITION
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AUTHORS
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G13533
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AR300453 Sequence
BD070551 Self-regu
AL6444 Xho-PstI fr
E02109 DNA sequenc
AJ249755 Homo sapi
108430 Sequence 5
107953 Sequence 6
E00702 CDNA encodi
103592 Synthetic h
10444 Sequence 2
A37272 Sequence 1
10444 Sequence 1
10819 Sequence 1
104169 Sequence 1
10419 Sequence 1
10419 Sequence 1
10419 Sequence 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G13533 SHGC-11076
                                                                             2, 2005, 18:55:28; Search time 783.946 Seconds (without alignments) 2657.805 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                          tcaaactggggcctccagaa.....actggggcctacagctttga
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                        4708233 seqs, 24227607955 residues
                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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107953
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Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
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length: 2000000000
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99b htg: *
99b on: *
99b ov: *
99b ph: *
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Perfect score:
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seconds seconds

94025, USA

PAT 12-JUN-2003

linear

FEATURES

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BD070551 787 bp DNA linear PAT 27-AUG-2002
Self-regulated apoptosis of inflammatory cells by gene therapy.
BD070551
                                                                                                                                                                                     1 (bases 1 to 787)
Tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: US 6537784-A 7 25-MAR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells by gene therapy
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PN JP 2001516210-A/13
PD 25-SEP-2001
PF 27-FEB-1998 JP 1998537909
PR 28-FEB-1997 US 60/032466
PI REVAI J TATAKE, STEVEN D MARLIN, RANDALL W BARTON PC A61K31/70,C07H21/04,C12N15/12,C12P19/34
CC Strandedness: Single;
CC TOPOlogy: Linear; Single;
CC TOPOlogy: Linear; Location/Qualifiers
FH Key 1 787
FT source /organism='Unidentified'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unidentified
unclassified.
1 (bases 1 to 787)
1 tatake, R.J., Marlin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory ce
Patent: JP 201516210-A 13 25-SEP-2001;
BOERRINGER INGELHEIM PHARMACEUTICALS INC
OS Unidentified
                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 43; DB 6; I
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 43; Conservative 0; Mismatches 0;
                                            DNA
                                        Sequence 7 from patent US 6537784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .787
/organism="unidentified"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                             AR300453.1 GI:31687895
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JP 2001516210-A/13.
                                                                                                                                                                                                                                                                                   1. .787
                                                                                                                                                                    Unclassified.
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                                                                                AR300453
                                                                                                                                  Unknown.
                                                                                                                                                         Unknown
   RESULT 3
AR300453
LOCUS
DEFINITION
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SOURCE
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ORGANISM
                                                                                                                                                   ORGANISM
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JOURNAL
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AUTHORS
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TITLE
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BD070551
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KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 787)

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PN JP 2002504381-A/7
PD 12-FRB-1999 JP 2000533579
PR 27-FEB-1999 US 60/076316
PI REVATI J TATAKE,STEVEN D MARLIN,RANDALL W BARTON PC C12N15/09,A61K31/7088,A61K48/00,A61P1/04,A61P3/10,A61P17/06, PC A61P25/00,
PC A61P29/00,A61P43/00,C12N9/64,C12Q1/68//C12N15/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tatake, R.J., Marin, S.D. and Barton, R.W.
Self-regulated apoptosis of inflammatory cells by gene therapy
Patent: JP 2002504381-A 7 12-FEB-2002;
BOGHRINGER INGELHEIM PHARMACEUTICALS INC
OS Homo sapiens (human)
PD 12-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Pred. No. 7.3e-07;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          TNF-alpha untranslated region
Key Location/Qualifiers

    400
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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organism="Homo sapiens"
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/db_xref="taxon:9606"
2.5 mM
50 mM
20 mM
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210. .375
210. .231
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JP 2002504381-A/7.
Homo sapiens (human)
Homo sapiens
                     KČl:
Trie-HCl:
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

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1. .>1047
/gene="TNF-alpha"
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/replace="t"
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/gene="TNF-alpha"
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               Best Local Similarity 100. Matches 43; Conservative
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Soma,G., Mizumo,D. and Tsuji,Y.
NOVEL DNA AND PRODUCTION THEREOF, NOVEL PLASMID HAVING SAME, NOVEL
POLYPEPTIDE AND PRODUCTION THEREOF AND NOVEL ANTINEOPLASTIC AGENT
PROM SAID POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I. Mizuno, D., Tsuji, Y. and Kobayashi, N.
Anti-aids preparation
Parent: EP 0450240-A 9 09-OCT-1991;
Soma, Gen-Ichiro; Mizuno, Den'ichi
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF 01-APR-1988 JP 1988081683
PI SOMA GENICHIRO, MIZUNO DENICHI, TSUJI YOSHIAKI PC
SUMIS/OO, AGNIXJ7/24, C07K13/OO, C12P21/O2, (C12P21/O2, C12R1:19); CC
strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: library=THP-1 cell;
FH Key
FH Key
FT mat_peptide >1. . <817
| /product='Anti-tumor polypeptide'.
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/product='Anti-tumor polypeptide'.
Location/Qualifiers
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100.0%; Pred. No. 7.3e-07;
cive 0; Mismatches 0;
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SOMA GENICHRO, MIZUNO DENICHI
PN JP 1989256390-A/1
PD 12-OCT-1989
                              Al6444 817 bp I
Xho-Petl fragment from THP-I cells.
                                                                                                                                                                                                                                                                                                           /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                             'organism="Homo sapiens"
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/organism="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
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Glycine max
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JP 1989256390-A/1.
                                                                                                             Homo sapiens (human)
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Best Local Similarity
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Homo sapiens TNF-alpha gene for tumor necrosis factor-alpha, 3'
UTR, country United Arab Emirates.
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Direct Submission
Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research
Submitted (24-SEP-1999) Farhan A.J., CID-Immunology Research
Submitted (34-SEP-1999) Farhan A.J., CID-Immunology Research
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mark, D.F., Lin, L.S., Lu, S.-D.Y. and Wang, A.M.
CYSTEINE-DEPLETED MUTEINS OF BIOLOGICALLY ACTIVE HUMAN TUMOR
NECROSIS FACTOR PROTEINS
PATENT: WO 8604606-A 5 14-AUG-1986;
Location/Qualifiers
1. .1275
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Identification of new rare variant of human TNF-alpha 3' UTR
Unpublished
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100.0%; Score 43; DB 9; Length 1047;
Best Local Similarity 100.0%; Pred. No. 7.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels (
100.0%; Score 43; DB 6; Length 817;
100.0%; Pred. No. 7.3e-07;
ive 0; Mismatches 0; Indels
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AJ249755.1 GI:6002308
TWF-alpha gene; tumor necrosis factor-alpha.
Homo sapiens (human)
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/db_xref="taxon:9606"
/country="United Arab Emirates"
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Sequence 5 from Patent WO 8604606.
108430
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hypothetical: No;
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mat_peptide
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I03610
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AUTHORS
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PD 26-FEB-1986
PP 05-JUL-1984 US 84 627959, 05-JUL-1984 US 84 628059, PR 05-JUL-1984 US 84 677257, 03-DEC-1984 US 84 677156, PR 03-DEC-1984 US 84 677257, 03-DEC-1984 US 84 677454 PI BARAA BUSHIYAN AGAWARU, DEBITSUDO BANNOCMAN GETSUDERU, PI SAN HII RII, PI GUREN EBAN NEDOUIN PI GARAANARU, DEBATSJ/12, AGIK35/12, AGIK35/12, AGIK35/12, AGIK35/14, AGIK35/14, AGIK35/14, AGIK35/16, C17N121/02, PC C07H21/04,
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1 (bases 1 to 1324)
Baraa,B.A., Debitsudo,B.G., San,H.R. and Guren,E.N.
Parent. 17 1986040221-A 1 26-FEB-1986;
GENENTECH INC
                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 1323)
Aggarwal, B.B., Lee, S.H., Goeddel, D.V. and Nedwin, G.E.
Tumor necrosis factor, methods for its preparation, compositions
containing it, DNA encoding it and assay method using such DNA
Patent: EP 0168214-A2 6 15-JAN-1986,
                                                                                            Gaps
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                                                           Length 1275;
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                                                                                                                 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA encoding human tumor necrosis factor.
                                                     Query Match 100.0%; Score 43; DB 6; Best Local Similarity 100.0%; Pred. No. 7e-07; Matches 43; Conservative 0; Mismatches 0
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="unassigned DNA"
                                                                                                                                                                                                                          1323 bp
Sequence 6 from Patent EP 0168214.
107953
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1. .1323
/organism="unknown"
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JP 1986040221-A/1
26-FEB-1986
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JP 1986040221-A/1.
Homo sapiens (human)
Homo sapiens
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Matches 43; Conservative
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1 (bases 1 to 1379)
Nobuhara,M., Kanamori,T., Nagase,Y., Nii,A., Morishita,H., Tohyama,J., Andoh,S. and Kurimoto,M.

The expression of human tumor necrosis factor in E. coli
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62. .532
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Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0
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*source: cell_type=promyelocytes;
*source: cell_line=HL-60;
*source: clone=lambda42-4, lambda16-4;
                                                                                                 Location/Qualifiers
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Aggarwal, B. B. and Lee, S.He.
Synergistic cytotoxic composition
Patent: US 4650674-A 2 17-MAR-1987;
Genentech, Inc.; So. San Francisco,
Location/Qualifiers
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Sequence 2 from Patent US 4650674.
103610
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tumor necrosis factor.
synthetic construct
synthetic construct
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Search completed: September 3, 2005, 01:14:21
Job time : 784.946 secs
                     Unknown.
Unclassified.
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/db_xref="d1:209486"
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DFAESGQVYFGIIAL"
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Nucleic Acids Symp. Ser. 17, 131-134 (1986)
87174864
3031624
Original source text: Altered human leukemic B-cell line Ball-1, cDNA to mRNA, clone pM324-346.
                                                                                                                                                                                                                                                                                                                                                 /note="Bynthetic tumor necrosis factor signal peptide"
400. .876
/product="synthetic tumor necrosis factor"
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/db_xref="taxon:32630"
/db_xref="synthetic tumor necrosis factor precursor"
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Woknown.

Unknown.

S 1 (bases 1 to 1465)

S Lin,L.S. and Yamamoto,R.

Purification method for tumor necrosis factor

AL Patent: US 4677197-A 2 30-UUN-1987;

Cetus Corporation; Emeryville, CA

Location/Qualifiers

1465
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Sequence 3 from Patent WO 8806625.
108863
108863.1 GI:588416
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Matches 43; Conservative
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Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels (
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1 (bases 1 to 1560)
Mark, D.F., Lin, L.S., Thomsom, J.W. and Yamamoto, R. ARGININE-DEPLETED HUMAN TUMOR NECROSIS FACTOR Patent: WO 8806625-A 3 07-SEP-1988;
Location/Qualifiers
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Vile, R.G. and Hart, I.R.
TUMOUR THERAPY
PATCHT: WO 9404196-A 12 03-MAR-1994;
IMP CANCER RES TECH (GB)
Location/Qualifiers

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Sequence 12 from Patent WO9404196.
A37272
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5.1.6
Compugen Ltd.
version 5
GenCore (c) 1993
       Copyright
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OM nucleic - nucleic search, using sw model

September 2, 2005, 18:45:43; Search time 131.925 Seconds (without alignments) 1929.494 Million cell updates/sec Run on:

US-09-801-371A-2

1 tcaaactggggcctccagaa.....actggggcctacagctttga 43 Title: Perfect score: Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4390206 seqs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

8780412

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseq 16Dec04:\* Database :

geneseqn1980s:\*
geneseqn1990s:\*
geneseqn2000s:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	ption		15 Seguence	Aaz99816 Cis-actin	Aaz20979 Human TNF	Adr12297 Human tum	Aan70075 Human ant	10 THP-1. 3	Aan91035 XhoI - Ps	72 Human ant	59 Part of g	sequence	Ade25716 Human cDN	Aan60363 Sequence	Aaa34963 Human ade	Aaf21085 Human low	Abz96779 Human nuc	Abd20628 Human pul	Aan80219 Sequence	Adq83817 Human tum	Aan60527 Sequence
	Description	Aaz998	Aaz99815	Aaz998	Aaz209.	Adr12	Aan700.	Aaq04340	Aan910	Aan70072	Aan90969	Aan60558	Ade25	Aan603	Aaa349(	Aaf210	Abz96	Abd20	Aan802	Adq83	Aan605;
	ΩI	AAZ99817	AAZ99815	AAZ99816	AAZ20979	ADR12297	AAN70075	AAQ04340	AAN91035	AAN70072	AAN90969	AAN60558	ADE25716	AAN60363	AAA34963	AAF21085	ABZ96779	ABD20628	AAN80219	ADQ83817	AAN60527
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Aan60557 Sequence Aca64836 Human TNF Ad£76346 Novel hum	Adi32003 Human cDN Ado19587 Human PRO		ຸິ	Aat15424 Human tum	Aan71307 Sequence	Aat31021 Human tum	Abk13195 Human tum	Aal53712 Tumour ne	Aad49644 Human tum	Adc35185 Human cDN	Aad63904 Human INF	Acc57575 Polynucle	Adr26040 Breast ca	Acf64375 Human TNF	Ade25664 Human cDN	Ads88038 Tumour tr	Adt08160 Human tum	Aaz20983 Chimeric	Aaz20984 Chimeric	Aav39005 TNF-alpha
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585 1 585 8 585 1	585 12	585 1	606 1	606 2	643 1	643 2	643 6	643 8	643 8	643 1(	643 1(	643 10	643 13	650 8	999	669 13	669	2270 2	570 2	634 2
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21 22 23	24 25	26		29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

AAZ99817 standard; RNA; 43 BP.

AAZ99817;

(first entry) 12-JUL-2000 

Cis-acting nucleotide sequence derived from human TNF-alpha.

Cis-acting sequence, intron removal, trans-acting factor; alpha-subunit; RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha; tumour necrosis factor alpha; TNF-alpha; gene therapy; 88.

Homo sapiens.

WO200014255-A1.

16-MAR-2000.

99WO-IL000483. 06-SEP-1999;

98IL-00126112 98IL-00126757 07-SEP-1998; 26-OCT-1998;

(YISS ) YISSUM RES & DEV CO.

Ben-Asouli Y; Jarrous N, Kaempfer R, Osman F,

WPI; 2000-257000/22.

Regulation of gene expression by mRNA splicing is carried out using a cis -acting nucleotide sequence controlled by phosphorylation of the alphasubunit of eukaryotic initiation factor 2.

Claim 5; Page 15; 75pp; English.

The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic

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initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumnour necrosis factor alpha (TNR-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (FRR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant therapeutic (e.g. an enzyme, hormone, growth factor, cytckine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a cis-acting nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a cis-acting nucleotide sequence which is which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eIP2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders splicing of precursor transcribte encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Regulation of gene expression by mRNA splicing is carried out using a cis -acting nucleotide sequence controlled by phosphorylation of the alphasubunit of eukaryotic initiation factor 2.
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                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of the stem loop of tumour necrosis factor-alpha gene.
                                                                                                                                                                                                                                                                                 100.0%; Score 43; DB 3; Length 43; 100.0%; Pred. No. 4.3e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
                                                                                                                                                                                                                                                                                                                                                                                      TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
                                                                                                                                                                                                                                            Sequence 43 BP; 10 A; 13 C; 11 G; 9 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                          43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-257000/22.
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                        Invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ99815;
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The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene witch that bursours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein finate capable of phosphorylating the alpha-subunit of enkaryotic initiation factor 2 (e1P2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3 untranslated region (3 UTR) of the human cumour necrosis factor alpha (TNY-alpha) gene, into another gene renders splicing of precursor transcripts encoded by that gene sensitive to the level of RNA-activated protein kinase (PKR) activity. The sequence can be used to transform host cells to regulate gene expression at the mRNA splicing level, for gene therapy, and to produce a recombinant the manner of the another protein the protein in the protein of produces a protein the protein the protein protein protein the protein of produces a protein. The
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therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural protein) or industrially or agriculturally applicable protein. The present sequence represents a fragment of the 3'UTR of human TNF-alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit; RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha; tumour necrosis factor alpha; INF-alpha; gene therapy; ss.
                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Cis-acting nucleotide sequence derived from human TNF-alpha.
                                                                                                                Length 50;
                                                                                                                      4.4e-07;
--- 0; Indels
                                                                                                                                                                                             43
                                                                                                                                                                                                                 S UCAAACUGGGGCCUCCAGAACUCACGGGGCCUACAGCUUGA 47
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                                                                          Sequence 50 BP; 12 A; 15 C; 12 G; 0 T; 11 U; 0 Other;
                                                                                                                                                                                             1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ben-Asouli Y;
                                                                                                                Score 43; DB
                                                                                                                                                     9; Mismatches
                                                                                                                                   Pred. No.
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                                                                                                                                                                                                                                                                                                                              AAZ99816 standard; RNA; 104 BP
                                                                                                              100.0%;
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98IL-00126757
                                                                                                                                   l Similarity 79.1%;
34; Conservative
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                                                                                                                                   Local Similarity
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                                                                                                                Query Match
                                                                                                                                                       Matches
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DB 3; Length 104;

100.0%; Score 43;

Query Match

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This sequence represents a human TNPalpha (tumour necrosis factor alpha)

3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were
constructed comprising at least one TNPalpha promoter enhancer region

(AAZ20975-Z20978), a TNPalpha promoter (AAZ20974), a DNA encoding
the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNPalpha

10'TNR sequence. TNPalpha is one of a number of cytokines produced by
the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNPalpha

2'UTR sequence. TNPalpha is one of a number of cytokines produced by
the sequence. TNPalpha is one of a number of cytokines in
thilamed tissue may be directly or indirectly responsible for
the acceptation of chronic inflammatory diseases. Introduction of the
conference of chronic inflammatory diseases. Introduction of the
the chimeric nucleotide to activated inflammatory cells causes them to
undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide
may be useful for treating inflammatory disorders such as multiple
sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus
the disease, lupus errythematosus, insulin-dependent (type I) diabetes
the construction of the construction of the colitis, the colitis the colitis than the chimeric nucleotide to activate of the colitis than the chimeric nucleotide to activate of the colitis than the chimeric nucleotide to activate of the colitis than the chimeric nucleotide to activate of the colitis than the chimeric nucleotide to activate of the colitis than 
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                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation; chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis; psoriasis; graft versus host disease; lupus erythematosus; diabetes; ankylosing spondylitis; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mellitus, ankylosing spondylitis, and in particular, rheumatoid arthritis. The use of such chimeric nuclectides offers simpler and cheaper long-term relief, in comparison with existing conventional
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  Se-07;
                                                                                                                         TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 47
                                                                                        1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCCTACAGCTTTGA 43
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llarity 100.0%; Pred. No. 6.8e-07;
Conservative 0; Mismatches 0;
pharmaceutical and invasive surgery methods
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                                      43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TNFalpha 3'UTR
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tes 43; Conserv
             Similarity
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Matches 43,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying modulators of untranslated region-dependent expression of a VEGF gene, useful for treating cancer, comprises contacting a compound with a cell or translation mixture containing a reporter gene linked to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                          Human tumour necrosis factor alpha 3'-untranslated region DNA.
                                                                                                                                                                                                                                                                                                                                  se; cytostatic; VEGF modulator; angiogenesis inhibitor;
UTR-dependent expression; vascular endothelial growth factor;
untranslated region; cancer; angiogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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100.0%;
100.0%;
                                                               ADR12297 standard; DNA; 792 BP.
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                                                                                                                                                                                                   21-OCT-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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20-JAN-1991
                                                                                                                                   ADR12297;
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RESULT 5
ADR12297
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                                                                                                                               SO CCC CCC CCC X S X L L L L X L X X L X L X L X L X X L X X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L X L
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Gaps

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226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

1 TCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCTTTGA 43

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Gaps

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Used in the prodn. of TNF prodn. agents. (Updated on 25-MAR-2003 to correct PD field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Section of gene for anticarcinogenic peptide. It is genomic DNA from THP-1 cells. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                  Length 817;
                                                                                Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 U; 0 Other;
                                                                                                                                                    0; Indels
                                                                                                                                                                                                         717 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 759
                                                                                                                                                                                   1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                       XhoI - PstI section of gene for anti-cancer peptide.
                                                                                                                 Query Match 100.0%; Score 43; DB 2; I
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 43; Conservative 0; Mismatches 0;
 Disclosure; Page ?; 26pp; Japanese
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(first entry)
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(first entry)
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ses 43; Conserv
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20-JAN-1991
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11-MAR-1990
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AAN91035
ID AAN9
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                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is an Xho-Pstl fragment of an anti-tumor protein. The polypeptide is cytotoxic to human tumor cells but not to normal cells. They are also cytotoxic to primary cell cultures obtained from metaetasis lesions of patients suffering from striated muscle tumors. They are also resistant to all chemotherapeutic agents. See also AAN70073-74, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intrinsic TNF prodn. derivation agents - contain primer and trigger, at least one of which has TNF activity.
                                                                                                                                                                                                                                                                                                                                   Anti-tumour polypeptide(8) - prepd. using recombinant DNA prepd. from genomic DNA of human acute leukaemia cell thp-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCAAACTGGGGCCTCCAGAACTCACTGGGGGCCTACAGCTTTGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acute leukaemia cell; THP-1; anti-tumour agent; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 43; DB 1; L 100.0%; Pred. No. 6.8e-07; trive 0; Mismatches 0;
Anti-tumor; cancer; cytotoxic; ss.
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                                                                                                                                                                               86JP-00024220.
                                                                                                                                  87EP-00400261
                                                                                                                                                                 86JP-00021302
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(first entry)
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Best Local Similarity 100.0
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-143138/19.
                                                                                                                                                                                                                                                                                                    WPI; 1987-336540/48
                                                                                                                                                                                                                                                                   Mizuno D, Soma GI;
                                                                                                                                                                                                                                (MIZU/) MIZUNO D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SOMA/) SOMA G.
                                 Homo sapiens
                                                                                                                                  04-FEB-1987;
                                                                                                                                                                                 07-FEB-1986;
17-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                04-FEB-1986;
                                                                                                 02-DEC-1987.
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21-SEP-1990
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                                                              EP247906-A.
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The sequence encoding TNF produced by the promyelocytic leukemia cell line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (80e AMR0552). Neither of the cysteine residues (69 and 101) in the TNF sequence appears to be involved in disulphide linkages. The patentors claim a novel synthetic mutein of a biologically active hTNF protein, having at least one cysteine residue free from a disulphide link and non-essential to the activity and having at least one of the cysteine residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New synthetic muteins of human tumour necrosis factor protein - are obtd.
by direct mutagenesis and retain antitumour activity.
                                               Gene for anticarcinogenic peptide. It is genomic DNA or cDNA from THP-1 cells. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser 69 in pAW731.
                                                                                                                                                                                                Gapa
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                                                                                                                           Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                    1099 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1141
                                                                                                                                                                                             0; Indels
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                                                                                                                                                        100.0%; Score 43; DB 1; L ilarity 100.0%; Pred. No. 7.3e-07; Conservative 0; Mismatches 0;
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1. .474
/*tag= a
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                    Fig 2; Page ?; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                         AAN60558 standard; DNA; 1275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antitumour; anticancer; ss
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                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            AAN60558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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                                                                                                                                                                                                                                                                                                                                                     Anti-tumour polypeptide(s) - prepd. using recombinant DNA prepd. from genomic DNA of human acute leukaemia cell thp-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1200,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agent, anti-cancer agent, THP-1 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 43; DB 1; L
100.0%; Pred. No. 7.3e-07;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Part of gene for anti-cancer peptide.
Anti-tumor; cancer; cytotoxic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 4; 63pp; English.
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                                                                                                                                                                       86JP-00021302.
86JP-00024220.
86JP-00169522.
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                                                                                                                                                                                                                                                                                 Soma GI;
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Matches 43; Conserv
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                                                                                                                                                                                                                                            ONUZIM (/NZIW)
                                                                                                                                                                       04-FEB-1986;
07-FEB-1986;
17-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SENG/) SEN G
                                  Homo sapiens
                                                                                                                                       04-FEB-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-2003
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11-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THP 1 cells.
                                                                                                   02-DEC-1987
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                                                                  EP247906-A
                                                                                                                                                                                                                                                                                 Mizuno D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAN90969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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**Gaps** 

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Indels

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Pred. No. 7.3e-07;

100.08;

Conservative

Mismatches

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Best Local Similarity
Matches 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a combination comprising several polymucleotides having any one of 127 sequences (31) such as the sequence of human calmon mRNA for KIAA0930 protein, leukotriene A4

Calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4

Dydrolase, human CII-142 protein mRNA, human K+ channel bat 2 subunit

mRNA, etc., and their complements. The cDNAs are differentially expressed

CC higopolysaccharide)-treated foam cells. Also included are

cobtaining an extended or full length gene from a library of nucleic acid

sequences, an expression vector containing the nucleic acids, a host cell

containing the vector, a purified polypeptide appearing as ADE25750 and

ADE25751, producing a protein by culturing the host cell, and a

composition comprising a protein by culturing the host cell, and a

composition comprision with a standard defines to the proteins. The foam cell-expression of one or more

composition comparison with a standard defines early, mid or late atherosclerosis and comparison with a standard defines early, mid or late composition with a standard defines early, mid or late to a high throughput screening of a library of molecules or compounds to cleanity a ligand which binds a polynucleotide. The library is chosen from DNA molecules, peptides, proteins and RNA molecules or compounds to identify at least one ligand which specifically binds a compounds to identify at least one ligand which specifically binds a compounds to identify at least one ligand which specifically binds a callowascular disorder. The foam cell-expressed nucleic acids are useful can elements on a microarray which can be used for detecting related components or microarray which can be used for detecting related as elements on a microarray which can be used for detecting related to a microarray which can be used to detecting related to a microarray which can be used for detecting related to a microarray which can be used to a microarray which can be used to a microarray which can be used to a microarray and a sequa
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                                                                                                                                                                                                                                                                                                                                                                                                 Human; 88; differential expression; foam cell; LPS; lipopolysaccharide; cardiovascular disease; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1279 BP; 293 A; 415 C; 323 G; 248 T; 0 U; 0 Other;
                                   697 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 739
        43
                                                                                                                                                                                                                                                                                                                                                  Human cDNA differentially expressed in foam cells #120.
     1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaser MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis. The present sequence rep
is upregulated in LPS treated foam cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 120; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porter JG,
                                                                                                                                                                                        ADE25716 standard; cDNA; 1279 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2002; 2002US-00247671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-SEP-2001; 2001US-0323784P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mikita T, Shiffman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-875398/81.
P-PSDB; ADE25778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                              29-JAN-2004
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                                                                                                                                                                                                                                          ADE25716;
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DB 10; Length 1279;

100.0%; Score 43;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encodes the pure human tumour necrosis factor, mutants of which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pure tumour necrosis factor and mutant forms - new DNA coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;
                        1081 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1123
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43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
  1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA

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    /*tag= b
    /label= Secretory leader peptide

                                                                                                                                                                                                                                                                       Sequence encoding human tumour necrosis factor.
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                                                                                                                                                                                                                                                                                                                     hTNF; tumour; cancer; interferon; da
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Fig 10; 90pp; English.
                                                                                                                                                 BP
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84US-00628059.
84US-00671156.
84US-00677157.
84US-00677257.
                                                                                                                                              AAN60363 standard; DNA; 1323
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                                                                                                                                                                                                                                  19-JUN-1991 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1986-015483/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAP60417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aggarwal BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-1985;
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1984;
03-DEC-1984;
03-DEC-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
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05-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP168214-A.
                                                                                                                                                                                        AAN60363;
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0; Indels

0; Mismatches

43; Conservative

Matches

us-09-801-371a-2.rng

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Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergy; antischoconstriction; inhibitor; antisflammatory; antiallergic; antischmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                        Human adenosine receptor related polynucleotide SEQ ID NO:2652
                                                                                                                                                         cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                  AAA34963 standard; DNA; 1324 BP
                                                                                                                                                                                                                                  99WO-US017712
                                                                                                                                                                                                                                                    98US-0095212P
                                                                                                                                                                                                                                                                     (UYEC-) UNIV EAST CAROLINA,
                                                      (first entry)
                                                                                                                                                                                                                                                                                                          WPI; 2000-205971/18.
                                                                                                                                                                                             WO200009525-A2.
                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                  03-AUG-1999;
                                                                                                                                                                                                                                                    03-AUG-1998;
                                                      28-JUL-2000
                                                                                                                                                                                                               24-FEB-2000
                                   AAA34963;
                                                                                                                                                                                                                                                                                         Nyce JW;
RESULT 14
         AAA3496:
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The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets conclete acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung diseases and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, compeded respiratory nypertension, emphysema, chronic obstructive timpeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the CONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing contain and inflammation. AAA1313 to AAA3312 represent the contain contains the contain contains the contains 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA12323 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence
New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 814-815; 1343pp; English.
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Length 1324;

Score 43; DB 3; | Pred. No. 7.4e-07;

100.0%; 100.0%;

Best Local Similarity

Query Match

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coligonucleotides and compositions (1) comparising them. In the antisense oligonucleotides and compositions (1) comparising them. In the antisense coligonucleotides the A is replaced by a 'Universal' or alternative base. (1) can have respiratory, bronchodilator, antilinflammatory, analgesis, communication in the antisense oligonucleotides and (1) can be used to down-regulate the expression and or activity of target polypeptides associated with undyrespiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific ensymes, binding proteins, adenosine receptors, bradykinin receptors, central cereptors, contral nervous system (CNS) and peripheral nervous and non-nervous system peptide correspitatory defensins, growth factors, vasoactive peptides and receptors, defensing proteins and malignancy associated proteins The antisense oligonucleotides may be used in this way to treat disorders antisense oligonucleotides may be used in this way to treat disorders and/or bronchoconstriction and/or lung inflammation, allergy(iss) and/or condition selected from pulmonary vasoconstriction, inflammation,
                                                                                                                                                                                                                                                                                                                               Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; respiratory obstruction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pain; cystic fibrosis; allergic rhinitis; constructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Low adenosine (A) content antisense oligonucleotides which do not trigge adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.
                                                                                                                                                                                                                                                                                      Human low adenosine antisense oligonucleotide related sequence #2652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes low adenosine (A) content antisense
                                            755 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 797
1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 887; 1592pp; English.
                                                                                                                                                      AAF21085 standard; DNA; 1324 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2000; 2000WO-US008020.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.
                                                                                                                                                                                                                                            14-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-679539/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; 88.
                                                                                                                                                                                                AAF21085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nyce JW;
                                                                                                          RESULT 15
                                                                                                                                    AAF2108
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CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary C (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary chypertension, emphysema, chronic obstructive pulmonary disease (COPD), CC pulmonary transplantation rejection, pulmonary infections, bronchitis, CC and/or cancer. AAF18434 to AAF21543 represent human polynuclectide CC fragments and antisense oligonuclectides used in the exemplification of CC the present invention XX

SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
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Search completed: September 3, 2005, 00:29:35 Job time : 132.925 secs

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0; Gaps

Query Match
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 43; Conservative 0; Mismatches 0; Indels (

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September 2, 2005, 23:36:03; Search time 983.15 Seconds (without alignments) 1664.816 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                         34239544 seqs, 19032134700 residues
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	T29839 EST97164 Hu			_	CA307429 UI-H-FT1-	_	Ξ	CD364761 UI-H-FT2-	_	CA308256 UI-H-FT1-	_	BQ007008 UI-H-EI1-	CA307062 UI-H-FT1-	CD364988 UI-H-FT2-	CA308777 UI-H-FT1-	CD368116 UI-H-FT1-	CA309711 UI-H-FT1-	CA310368 UI-H-FT1-	CD368929 UI-H-FT1-	CA309509 UI-H-FT1-	CD366187 UI-H-FT1-	CA306559 UI-H-FT1-	CD240146 DTL3P2G5	AL543083 AL543083
SUMMARIES	QI.	T29839	BX118951	CB528492	CD370363	CA307429	CD367676	CA307225	CD364761	CD368142	CA308256	CB528694	BQ007008	CA307062	CD364988	CA308777	CD368116	CA309711	CA310368	CD368929	CA309509	CD366187	CA306559	CD240146	AL543083
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	Query Match	100.0	100.0	100.0	100.0	100.0	0.001	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	0.00
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	Score	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
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COMMENT

Contact: Venter, JC
Contact: Venter, JC
The Institute for Genomic Research
912 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699423
Email: tdbinfowtdb.tigr.org
Email: tdbinfowtdb.tigr.org
Enclose availability, additional sequence and expression information related to this EST, please contact the TIGR Database (tdbinfowtdb.tigr.org)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .248

source

FEATURES

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RESULT 3
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E. (bases I to 474)

E. Losses I to 474)

E. Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M., Radelof, U., Schneider, D. and Korn, B.

Human Unigeneset - RZPD3

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD, IMAG9981124300.

RZPDIIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDIB) No.972)

http://www.rzpd.de/CloneGards/cgi-
bin/showLib.pl.cgi/response?libNo-972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                BX118951 Soares fetal heart NbHH19W Homo sapiens CDNA clone IMAGD998L124300 ; IMAGE:1693595, mRNA sequence.
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC. Location/Qualifiers
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                                                                                                                                       Length 248;
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hes 0; Indels
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iive 0; Mismatches
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/tissue_type="Alvedar Macrophage"
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EROR I; Site_2: Not I;
NCI CGAP FT2: sa a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different moil 0, 3 hours; Rababella moil 0, 3 hours; Rababella moil 0, 3 hours; Adenovirus moil 500, 3 hours; A denovirus moil 500, 3 hours; Wt adenovirus the library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the Univerty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
thtp://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
sequence: 1-29, >AT rich#Low_complexity (matched compliment)
205-279, >(TAAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA-Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB528492 630 bp mRNA linear EST 05-AUG-2004 UI-H-FT2-bjd-e-20-01.sl NCI CGAP_FT2 Homo sapiens cDNA clone UI-H-FT2-bjd-e-20-0-UI 3', mRNA sequence.
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Query Match 100.0%; Score 43; DB 5; I Best Local Similarity 100.0%; Pred. No. 2.8e-05; Matches 43; Conservative 0; Mismatches 0;
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NCI_CGAP_FII is a normalized cDNA library constructed from a pool of 81 kNA samples from Alveolar Marcophages
challenged with different treatments. The mRNA samples were mixture of these conditions themse refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 3 hours; LPS 100 ng/ml, 3 hours; Rabeislal moi 10, 24 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 3 hours; Adenoviral moi 10, 3 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 3 hours; Adenovirus moi 500, 3 hours; Adenovirus + LPS 3 hours; Ad one of the LPS 3 hours; Adenovirus + LPS 3 hours; Adenovirus + LPS 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD370363 645 bp mRNA linear EST 05-AUG-2004
UI-H-FTI-bkb-n-03-0-UI.81 NCI CGAP FTI Homo sapiens cDNA clone
UI-H-FTI-bkb-n-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Experiencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this CDNA
Seg primer: M13 FORWARD
POLYA=Yes.
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(Dases 1 to 645)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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of Iowa.
TAG_TISSUE-Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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                                                                                                                                                                                       100.0%; Score 43; DB 6; L
100.0%; Pred. No. 2.8e-05;
iive 0; Mismatches 0;
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CD370363.1 GI:31154453
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Homo sapiens
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Matches 43; Conservative
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normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pyTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT).18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG_IISUE-H-FTI TAG_EBCCATGCCG."
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Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cond Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@wlowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, ... TRAAA) n#Simple_repeat
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UI-H-FTI-bic-i-01-0-UI.sl NCI CGAP_FT1 Homo sapiens cDNA clone
UI.H-FTI-bic-i-01-0-UI 3', mRNA sequence.
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR i; Site_2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of
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hours; wt adenovirus + LPS 24 hours. The library was
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/tissue_type="Alveolar Macrophage"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 6; I
Pred. No. 2.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 43; Do Best Local Similarity 100.0%; Pred. No. 2.89
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/db_xref="taxon:9606"
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Seq primer: M13 FORWARD
POLYA=Yes.
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Unpublished (1997)
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the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Rlebsiella moi 10, 3 hours; Rlebsiella moi 10, 24 hours; Rlebsiella moi 10, 24 hours; Rlebsiella moi 10, 3 hours; Rlebsiella moi 10, 24 hours; Rlebsiella moi 10, 3 hours; Rlebsiella moi 10, 24 hours; Raph aureus moi 10, 3 hours; Agaph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CWV eGFP), moi 500, 24 hours; Ad vector + LPS 3 hours; Wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Wt adenovirus moi 500, 3 hours; Wt adenovirus moi 500, 24 hours; Wt adenovirus + LPS 24 hours; The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is convenient to the langue was provided by Dr. Gary W.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eu 1, Ubases 1 to 688)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

L Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at thtp://genome.uiowa.edu/distribution/Cgap.html
The following repetitive elements were found in this CDNA sequence: 69-143, «TiPAA)n#Simple_repeat
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NCI_CGAP_FT1 Homo sapiens cDNA clone
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/tissue_type="Alveolar Macrophage"
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UI-H-FT1-bjr-1-14-0-UI 3', mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.(
Matches 43; Conservative
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CD367676/c
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AUTHORS
TITLE
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/dev stage="Adult"
/lab_host="DH108 (Life Technologies)"
/clonellab="NCI_CGAP_FTI"
/clonellab="NCI_CGAP_FTI"
/note="Organ: Lung, Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized CNNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions, other donor macrophages in different conditions, other donor macrophages in different control of hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 4 hours; Adenoviral vector (AdS CRV eGFP), moi 500, 3 hours; Adenoviral vector (AdS CRV eGFP), moi 500, 3 hours; Ad vector + LPS 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; wt adenovirus + LPS 24 hours; The library was normalized according to Bounks; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours; The library was normalized according to Bounded to an EcoR I adaptor, digested with Not I, and cloned directionally into primed with an oligo-dT primer containing a Not I site Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into prime Hoursing Hours; was provided by Dr. Gary W. Hunninghake of first-strand cDNA contains a library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE-Alman Lung Alveolar Macrophage
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UI-H-FT1-bhu-n-04-0-UI.81 NCI CGAP_FT1 Homo sapiens cDNA clone
UI-H-FT1-bhu-n-04-0-UI 3', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
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TAG_SEQ=GGCCATGCCG"
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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CD368142/c
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                                                                                                                                                                                                                                                                                                                                                   /dev stage="Adult"
//lab_host="PHOB (Life Technologies)"
//clone_lib="NCI_CGAP_FTI"
//lab_host="PHOB (Life Technologies)"
//clone_lib="NCI_CGAP_FTI"
//note="Organ: Lung, Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: ECOR I; Site_2: Not I;
NCI_CGAP_FTI is a normalized cDNA library conserucced from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; Capp hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; Rlebsiella
moi 10, 3 hours; Raba aureus moi 10, 24 hours; Staph aureus
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; At adenovirus moi 500,
3 hours; Ad vector + LPS 24 hours; Wt adenovirus moi 500,
3 hours; Wt adenovirus + LPS 24 hours; At alenovirus HDS 3
hours; wt adenovirus + LPS 24 hours; At alenovirus HDS 3
hours; wt adenovirus + LPS 24 hours; At adenovirus HDS 3
hours; wt adenovirus + LPS 24 hours; At adenovirus HDS 3
hours; wt adenovirus + LPS 24 hours; At adenovirus HDS 3
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hours; wt adenovirus + LPS 24 hours; At adenovirus HDS 3
hours; wt adenovirus + LPS 24 hours; At adenovirus HDS 3
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hours; wt adenovirus + LPS 24 hours; At adenovirus HDS 3
hours; wt adenovirus + LP
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UI-H-FT2-bjm-j-11-0-UI.81 NCI CGAP_FT2 Homo sapiens CDNA clone
UI-H-FT2-bjm-j-11-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 699)
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The following repetitive elements were found in this cDNA sequence: 296-370, >(TAAA)n#Simple_repeat Seq primer: M13 FORWARD POLYA=Yes.
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                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="taxon:960"
/clone="UI-H-FT1-bhu-n-04-0-UI"
/tissue_type="Alveolar Macrophage"
                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_LIB=UI-H-FT1
TAG_SEQ=GCCATGCCG"
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Homo sapiens
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KEYWORDS
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/downer="UT-H-FT2-D00"
/(Jone="UT-H-FT2-D00"-j-11-0-UI"
/(issue_type="Alveolar Macrophage"
/(dev_stage="Alveolar Macrophage"
/(dev_stage="Alveolar Macrophage"
/(lab_host="Utolar Macrophage")
/(lab RNA samples from Alveolar Macrophage")
/(lab RNA samples from Alveolar Macrophage")
/(lab RNA samples from Alveolar Macrophage")
/(lab RNA samples from Macrophage")
/(lab RNA samples were cultured in some of the conditions, other donor macrophages in different conditions, other donor scontrol 3 hours; Kabbaiella moi 10, 3 hours; Kabbaiella moi 10, 24 hours; Machoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Wt adenovirus moi 10, 3 hours; Wt adenovirus hours; Wt adenovirus hours; Mt adenovirus h
               Induct: Sobert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution Information can be found at
http://genome.uiowa.edu/distribution/ogap.html
The following repetitive elements were found in this cDNA
sequence: 296-370, >(TAAA)n#Simple_repeat
Seg primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
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TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Homo sapiens
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Numor Gene Index
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Homo sapiens
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DEFINITION
                                           RESULT 10
CA308256/c
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                                                                                                                                                                                                                     ACCESSION
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/tissue_type="Alyeolar Macrophage"
/dev_stage="Adult"
/lab host="Milto" (Life Technologies)"
/lab host="Milto" (Life Technologies)"
/clone lib="NCI_CGAP_FTI"
/note="Organ: Lung, Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of BI RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples
were a mixture of these conditions (times refer to
incubations following isolation by bronchoalveolar lavage)
(some normal donor macrophages were cultured in some of
the conditions, other donor macrophages in different
conditions). The mRNA samples were pooled for library
construction. Control 0 hours; control 3 hours; control 24
hours; LBS 100 ng/ml, 3 hours; LBS 100 ng/ml, 24 hours; Chebsiella
moi 10, 3 hours; Rebbiella moi 10, 24 hours; Rlebsiella
moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenoviral vector
(Ad5 CMV eGFP), moi 500, 24 hours; Adenovirus moi 500,
3 hours; Ad vector + LBS 24 hours; The library was
normalized according to Bonaldo, Lennon and Soares Genome
Research, 6:191-806, 1996. Fitst strand cDNA synthesis was
primed with an oligo-dT primer containing a Not I site.
Double stranded cDNA was ligated to an EcoR I adaptor,
digested with an oligo-dT primer containing a library tag
sequence that is located between the Not I site and the
(GT) 18 tail. The sequence tag for this library is
GGCCATGCCG. The tissue was provided by Dr. Gary W.
The Trest-etuman Library and the research of the University of Iowa.
The research of the University of Iowa.
The research of the University of Iowa.
                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Gary W. Hunninghake, U of I

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.ulowa.edu/distribution/cgap.html

The following repetitive elements were found in this CDNA

Seq primer: M13 FORWARD

POLYA-Yes.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
1 (Dases 1 to 703)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-CGAP Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAG TISSUE=Human Lung Alveolar Macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="UI-H-FT1-bjv-e-20-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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TAG_SEQ=GGCCATGCCG"
                                                                    REFERENCE
AUTHORS
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                                                                                                                                            TITLE
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0; Gaps

100.0%; Score 43; DB 6; Length 703; 100.0%; Pred. No. 2.9e-05; ive 0; Mismatches 0; Indels

43; Conservative

Matches

Best Local Similarity

Query Match

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CA108256

CA1082
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Homo sapiens
                                                                                                                                                                                                                 Query Match
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KEYWORDS
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/ / Organism="homo saptens"
/ / Organism="homo saptens"
/ / Clone="Utl-FT2-bjd-1-22-0-UI"
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/ Lissue
/ Lissue_type="NOI CGAP_FT2"
/ Lissue
/ Lissue_type="NOI CGAP_FT2"
/ Lissue
                                                                                                                                                                                                                                                                                                                                                                                                                             719 bp mRNA linear EST 05-AUG-2004
NCI_CGAP_FT2 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryoca, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 719)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                     Gaps
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                                                                                         Length 713;
                                                                                     Query Match 100.0%; Score 43; DB 6; Length 71
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 43; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                    590 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 548
                                                                                                                                                                                                              1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                          UI-H-FT2-bjd-1-22-0-UI.s1 NCI CGAP FT2 Ho
UI-H-FT2-bjd-1-22-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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TAG_SEQ=GGCCATGCCG'
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CB528694.1 GI:29388630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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AUTHORS
TITLE
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/clone="InkGE:5846517"
/tissue_type="Chondrosarcoma"
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/dev_stage="Chondrosarcoma"
/lab_host="Disput | Life Technologies" |
/clone_lib="NCI_CGAP_EII"
/clone_lib="NCI_CGAP_E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            722 bp mRNA linear EST 26-MAR-2002 UI-H-EII-azb-j-22-0-UI.sl NCI_CGAP_EII Homo sapiens cDNA clone IMAGE:5846517 3', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://imags.llnl.gov
The following repetitive elements were found in this cDNA sequence: 29-371, >(TAAA) n#Simple_repeat
Seq primer: Mil FORWARD
POLYA-YES.
was provided by Dr. Gary W. Hunninghake of the University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I Chases I to 732, NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
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                                                                                                                                                                                                                                                                                                                                                                  Length 719;
                                                                                        TAG_LIB=UI-H-FT2
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       588 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 43; DB 6; I
100.0%; Pred. No. 2.9e-05;
tive 0; Mismatches 0;
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TAG_LIB=UI-H-EI1
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (1997)
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Matches 43; Conservative
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Similarity
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Best Local Simil
Matches 43; C
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AUTHORS
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//do_type="mRNA"
//do_type="mRNA"
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/fab_host="DHIOB (Life Technologies)"
//lone=lib="NCI_CGAP_FTI"
//lone=lib="NCI_CGAP_FTI"
//note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EccR I; Site 2: Not I;
NCI_CGAP_FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 3 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 4 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 24 hours; Adenoviral vector (AdS CMV eGFP), moi 500, 24 hours; wt adenovirus mis 500, 3 hours; wt adenovirus + LPS 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Producement: Dr. Gary W. Hunninghake, U of I
Tissue Producement: Dr. Gary W. Hunninghake, U of I
Tissue Producement: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 295-365, > (TAAA) n#Simple_repeat
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                             CA307062 722 bp mRNA linear BST 05-AUG-2004 UI-H-FTI-bhu-o-04-0-UI.81 NCI CGAP FT1 Homo sapiens cDNA clone UI-H-FTI-bhu-o-04-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (basea 1 to 722)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                       Gaps
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           Length 722;
                                                                                0; Indels
                                                                                                                                                                                               591 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGGTTTGA 549
                                                                                                                                                        1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
100.0%; Score 43; DB 5; L
100.0%; Pred. No. 2.9e-05;
tive 0; Mismatches 0;
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EST.
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Homo sapiens
                                                                            43; Conservative
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Unpublished (1997)
                                          Best Local Similarity
Matches 43; Conserv
       Query Match
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CA307062/c
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TITLE
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KEYWORDS
SOURCE
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FEATURES

COMMENT

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/mol type="mRNN"
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// Lissue type="Alvedar Macrophage"
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// Clone 11b="MCI CdAF FT2"
// Clone 11b="MCI CdAF FT2"
// Clone 12b="MCI CdAF FT2"
// CdAP FT2 is a subtracted cDNA library Constructed from modified polylinker; Site 1: EcoR I; Site 2: Not I;
// CdAP FT2 is a subtracted cDNA library Constructed from a pool of 81 RNA samples from Alveolar Macrophages
challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)
// Some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions. The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LBS 100 ng/ml, 3 hours; RB hours; RB NA 10 ng/ml, 34 hours; RB LBS RDA 10 ng/ml, 24 hours; RB LBS RDA 10 ng/ml, 24 hours; RB LBS RDA 10 ng/ml, 24 hours;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD364988 172-bjn-c-04-0-UI.sl NCI CGAP_FT2 Homo Bapiens CDNA clone UI-H-FT2-bjn-c-04-0-UI.sl NCI CGAP_FT2 Homo Bapiens CDNA clone UI-H-FT2-bjn-c-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbe-remail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cond Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/cgap.html
The following repetitive elements were found in this cDNA
Sequence: 297-371, > (TAAA) n#Simple_repeat
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea I to 722) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
digested with Not I, and cloned directionally into pr773 Pac vector. The oligonucleotide used to prime the synthesis of first-etrand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 722;
                                                                                                                                                                                                                                                             TAG TISSUB-Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   589 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 6; I
Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD364988.1 GI:31149078
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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us-09-801-371a-2.rst

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/clone lib= NCIC (GAP FTI" note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECoR 1: Site 2: Not 1: NCI CGAP FTI is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA308777 1723 bp mRNA linear EST 05-AUG-2004 UI-H-FTI-bhy-b-23-0-UI.sl NCI CGAP FT1 Homo sapiens cDNA clone UI-H-FT1-bhy-b-23-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
TONA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (AdS CWV eGPP), moi 500, 3 hours; Adenoviral vector (AdS CWV eGPP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; wt adenovirus # LPS 3 hours; wt adenovirus + LPS 24 hours; wt adenovirus + LPS 24 hours; The library was subtracted according to Bonaldo, Lennon was provided by Dr. Gary W. Hunninghake of the University of Iowa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 723) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Dr. M. Bento Soares, bento-soares@ulowa.edu
The following repetitive elements were found in this cDNA
sequence: 297-371, >(TAAA)n#Simple_repeat
Seq primer: MI3 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 43; DB 6; Length 722; 100.0%; Pred. No. 2.9e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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/lab_host="DH10B (Life Technologies)"
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/mol_type="mRNA"
/bd_xref="taxon:9606"
/clone="UI-H-FT1-bhy-b-23-0-UI"
/tissue_type="Alveolar Macrophage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              TAG_SEQ=GGCCATGCCG"
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CA308777.1 GI:24471831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
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CA308777/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
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construction. Control 0 hours; control 3 hours; control 24 hours; control 10 hours; control 24 hours; control 24 hours; LPS 100 ng/ml, 24 hours; Rlebsialla moi 10, 3 hours; Rlebsialla moi 10, 3 hours; Rlebsialla moi 10, 24 hours; Rlebsialla moi 10, 3 hours; Rebsialla moi 10, 3 hours; Rebsialla moi 10, 24 hours; Adenoviral vector (AdS CRW eGFP), moi 500, 3 hours; Adenoviral vector (AdS CRW eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 3 hours; wt adenovirus + LPS 24 hours; The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with Not I, and cloned directionally into digested with Not I, and cloned directionally into py773-Pac vector. The oligonuclectide used to prime the synthesis of first-ekrand cDNA contains a library tag sequence that is located between the Not I site and the (AT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Huminghake of the University of Iowar.
conditions). The mRNA samples were pooled for library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAG_TISSUE=Human Lung Alveolar Macrophage TAG_LIB=UI-H-FT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_SEQ=GGCCATGCCG"
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ORIGIN

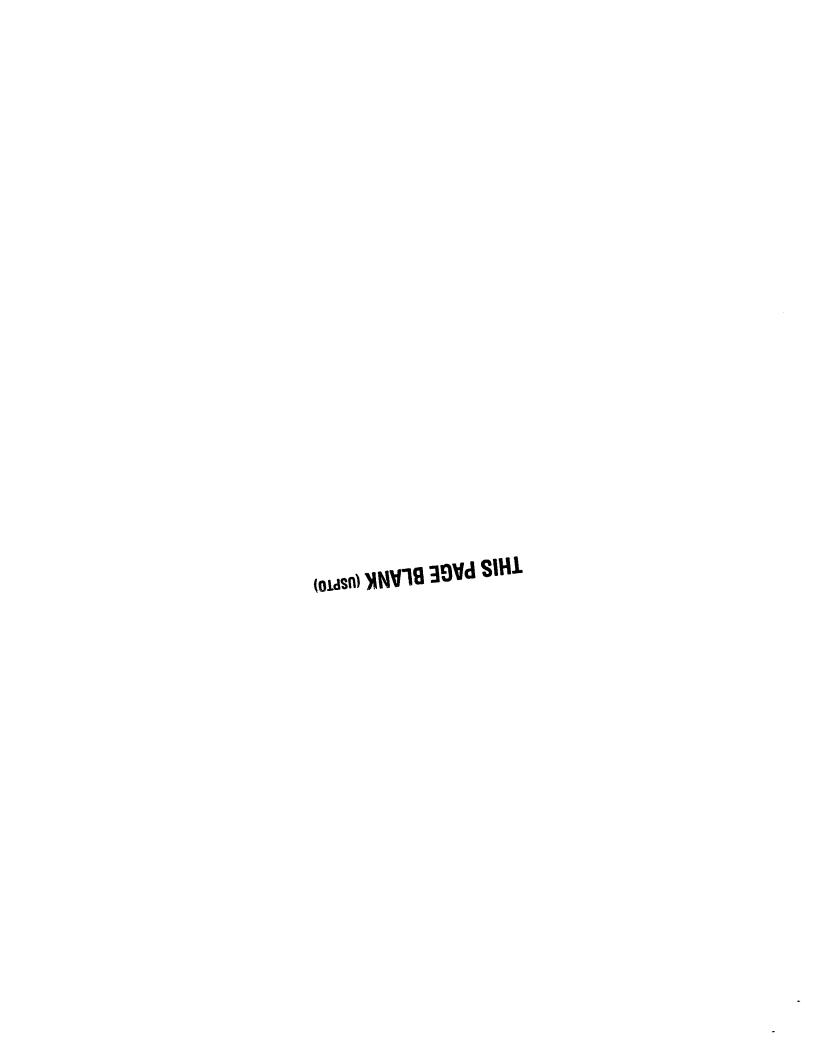
8 원 ORIGIN

Gaps ö ch 100.0%; Score 43; DB 6; Length 723; Il Similarity 100.0%; Pred. No. 2.9e-05; 43; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 43; Conserv

ö

Search completed: September 3, 2005, 02:11:42 Job time : 985.15 secs

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Sequence 2202, Ap Sequence 1777, Ap Sequence 978, App Sequence 716, App Sequence 114, App Sequence 11, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

Sequence Seq

Sequence

OM nucleic

Run on:

Sequence:

Searched:

Database

Result

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Score 43; DB 4; Length 787; Pred. No. 5.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09032297A
Patent No. 6525184
GENERAL INFORMATION:
APPLICANT: Revari J. Tatake, Steven D. Marlin and
APPLICANT: Revari J. Tatake, Steven D. Marlin and
TITLE OF INVENTION: Self-Regulated Apoptosis of
Inflammatory Cells by Gene Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPERSONDERING ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: Booklidgebury Road, P.O. Box 368
CITY: Ridgefield
STATE: Connecticut
COUNTRY: Ridgefield
STATE: Connecticut
CONPERS: CONNECTICUT
COMPUTER: Noise States of America
ZIP: 06877-0368
COMPUTER: TEMP PC
COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: IBM PC
COMPUTER: BM PC
COMPUTER: Word Processing
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,297A
FILING DATE: 27-Feb-1998
CLASSIFICATION NUMBER: GO/038,266
FILING DATE: 28-FEB-97
ATTORNEY/AGENT INFORMATION:
NAME: ROBERT NUMBER: 25089
REFERENCE/DOCKET NUMBER: 25089
US-09-949-016-12620

US-09-949-016-12081

PCT-US95-12987-1

PCT-US95-12987-3

US-09-705-400-64

US-09-949-016-11808

US-09-949-016-11808

US-09-949-016-11808

US-09-949-016-1777

US-09-621-976-2765

US-09-621-976-714

US-09-621-976-714

US-09-621-976-718

US-09-621-976-7185

US-09-621-976-7185

US-09-61-976-2765

US-09-91-976-2765

US-09-91-976-276

US-09-91-976-276

US-09-91-976-276

US-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 203-791-6183
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DESCRIPTION: DNA
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636591
636591
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Best Local Similarity
     RESULT 1
US-09-032-297A-13
                                                                                                                                                                                                                          Sequence 1329, Ap
Sequence 5156, Ap
Sequence 36, Appl
Sequence 4, Appli
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126, App
3, Appli
12341, A
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34, Appl
16898, A
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                                                                                                                                                                                       2, 2005, 13:14:57; Search time 175.51 Seconds (without alignments) 400.888 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34,
Sequence 1689
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                               version 5.1.6
- 2005 Compugen Ltd.
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US-09-229-151C-7
US-09-949-016-5156
US-09-949-016-5156
US-09-505-250-4
US-09-229-151C-14
US-09-229-151C-14
US-09-166-1186-1
US-09-166-1186-1
US-09-949-016-16898
US-09-949-016-16898
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US-09-949-016-15997
US-09-949-016-15298
US-09-949-016-15298
US-09-949-016-15298
US-09-949-016-15298
US-09-949-016-15741
US-09-949-016-157730
US-09-949-016-157731
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US-09-949-016-12621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1202784 segs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                               GenCore (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                               US-09-801-371A-2
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                                                      Copyright
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SERVERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US /09/949, 016

CURRENT FILING DATE: 2000-04-14

PRIOR PELICATION NUMBER: 60/237, 768

PRIOR PELICATION NUMBER: 60/237, 768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHARE: FESTERE TESTERE TO WINDOWS VERSION 4.0

LENGTH: 1587
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Pred. No. 6e-08;
                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 43; DB 4; Length 1585;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049
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APPLICANT: Bishopric, Nanette H.
APPLICANT: Bishopric, Nanette H.
APPLICANT: Murphy, Brian
APPLICANT: Green, Christopher J.
APPLICANT: Green, Christopher J.
TITLE OF INVENTION: Therapeutic Constructs
TITLE OF INVENTION: Therapeutic Constructs
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Scot.
100.0%; Pred. No. ve.
              REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1329:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5156, Application US/09949016
Patent No. 6812339
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  REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 43; Conservative
                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                            LIBRARY: GENBANK
CLONE: 9339737
US-09-023-655-1329
                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5156
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APPLICANT: Tatake, Revati J.
APPLICANT: Tatake, Revati J.
APPLICANT: Tatake, Revati J.
APPLICANT: Barton, Randall W.
APPLICANT: Barton, Randall W.
APPLICANT: Barton Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy FILE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy FILE REPERENCE: 9/137
CURRENT PILING DATE: 1999-01-12
RICR APPLICATION NUMBER: US 60/076,316
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 2.0
SEQ ID NO 7
LENGTH: 787
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Patent No. 6607879
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Suan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCES. 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
  Gaps
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0; Indels
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                                                                                         226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268
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COMPUTER READABLE FORM:
MEDLUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                           1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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100.0%; Pred. No. 5.2e-08;
Live 0; Mismatches 0;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/09/023,655
                                                                                                                                                                                                      Sequence 7, Application US/09229151C
Patent No. 6537784
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TTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0
43; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-023-655-1329
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; NAME/KEY: CDS
; LOCATION: (153)...(854)
US-09-505-250-4
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ORGANISM: Human
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ORGANISM: Human
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APPLICANT: Rosen, Glenn
APPLICANT: Rose, Peter
TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
TITLE OF INVENTION: Triptolides and Death Domain Ligands
FILE REPERENCE: SUN-109FRV2
CURRENT APPLICATION NUMBER: US/09/505,250A
CURRENT FILING DATE: 2000-02-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASELSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/880,342
FILING DATE: 23-JUN-1997
CLASSIPICATION NUMBER: PCT/IB95/0096
FILING DATE: 13-JUN-1997
CLASSIPICATION DATA:

APPLICATION NUMBER: PCT/IB95/0096
FILING DATE: 13-MOV-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/365,486
FILING DATE: 13-MOV-1994
ATTORNEY/AGENT INFORMATION:

NAMME: Sholtz, Charles K.

REGISTRATION NUMBER: 8255-0018.30
TELEPHONE: (415) 324-0880
TELEPHONE: (415) 324-0866
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
                                                                                                      ZIP: 94306
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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153..851
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ORGANISM: H. sapiens
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US-08-880-342-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                               CITY: Pal
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 1643
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SEQUENCE 14 Application US/09229151C

| SEGNERAL INFORMATION:
| APPLICANT: Tatake, Revati J. |
| APPLICANT: Barton, Randall W. |
| TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy FILE REFERENCE: 9/137 |
| CURRENT APPLICATION NUMBER: US/09/229,151C |
| PRIOR APPLICATION NUMBER: US 60/076,316 |
| PRIOR PILING DATE: 1999-02-27 |
| NUMBER OF SEQ ID NOS: 15 |
| SOFTWARE: Patentin version 2.0 |
| SEQ ID NO 14 |
| LENGTH: 2570 |
| LENGTH: 2570 |
| SOFTWARE: Patentin version 2.0 |
| LENGTH: 2570 |
| SOFTWARE: Patentin version 2.0 |
| CONTENT APPLICATION NUMBER: Patentin version 2.0 |
| SEQ ID NO 14 |
| LENGTH: 2570 |
| CONTENT APPLICATION NUMBER: Patentin version 2.0 |
| CONTENT APPLICATION NUMBER: PATENTIN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09229151C

Sequence 13, Application US/09229151C

Sequence 13, Application US/09229151C

Barton No. 6537784

GENERAL INFORMATION:

APPLICANT: Tatake, Revati J.

APPLICANT: Tatake, Revati J.

APPLICANT: Barton, Randall W.

TITLE OF INVENTION: Self-Regulated Apoptogia of Inflammatory Cells by Gene Therapy
FILE REPREBUCE: 9/137

CURRENT APPLICATION NUMBER: US/09/229,151C

CURRENT FILING DATE: 1999-01-12

PRIOR FILING DATE: 1998-02-27

PRIOR FILING DATE: 1998-02-27

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 2.0

SEQ ID NO 13.
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Query Match
100.0%; Score 43; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                            1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116
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US-09-229-151C-14
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; OTHER INFORMATION: chimeric gene : -706TNPpGB3'UTR
US-09-229-151C-13
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100.0%; Score 43; DB 4; I
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches 43; Conservative 0; Mismatches 0;
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2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854
                                                                               RESULT 10
US-09-313-932-1
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NAME/KEY: :
LOCATION:
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LOCATION:
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APPLICANT: Baker, Brenda
APPLICANT: Bennett, C. Frank
APPLICANT: Butler, Madeline M.
APPLICANT: Butler, Madeline M.
APPLICANT: Butler, Madeline M.
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE MODULATION OF TNF-a EXPRESSION
FILE REFERENCE: ISPH-0322
CURRENT APPLICATION NUMBER: US/09/166,186A
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 250
SEQ ID NO: 250
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LOCATION: (2171)...(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Sakaguchi, D.
AUTHORS: Jarrett-Nedwin, J.
AUTHORS: Geoddel, D.V.
AUTHORS: Geoddel, D.V.
AUTHORS: Gray, P.W.
TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, TITLE: homology and chromosomal localization
JOURNAL: Aucheic Acids Res.
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                                          2009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2051
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Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 43; Conservative 0; Mismatches 0; Indels
                      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA
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LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
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DATABASE ENTRY DATE: 1997-02-17
                                                                                                                                        US-09-166-186-1; Sequence 1, Application US/09166186A; Patent No. 6080580
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(1635)..(1821)
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(1822)..(1869)
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LOCATION: (1870)..(2070)
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(982)..(1588)
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NAME/KEY: exon
LOCATION: (615)..(981)
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DATE: 1985-09-11
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LOCATION:
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Gaps
Sequence 1, Application US/09313932A

Patent No. 6228642

GENERAL INFORMATION:
APPLICANT: Barer, Brenda

APPLICANT: Benett, C. Frank
APPLICANT: Butler, Madeline M.
TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDE MODULATION OF TNF-
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: ISPH-0356
CURRENT APPLICATION NUMBER: US/09/313,932A
CURRENT FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 501
SEQ ID NO.
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TITLE: Human lymphotcoxin and tumor necrosis factor genes:
TITLE: structure, homology and chromosomal localization
JOURNAL: Nucleic Acids Res.
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100.0%; Score 43; DB 3; I
Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 43; Conservative 0; Mismatches 0;
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DATE: 1985-09-11

DATE: 1985-09-11

DATE: 1985-09-11

JEAN PAGES ACCESSION NUMBER: X02910 Genbank

US-09-313-932-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (2171)...(3381)
PUBLICATION INFORMATION:
AUTHORS: Nedwin, G.E.
AUTHORS: Naylor, S.L.
AUTHORS: Sakaguchi, A.Y.
AUTHORS: Smith, D.
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(1822)..(1869)
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NAME/KEY: intron
LOCATION: (1870)..(2070)
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(1635)..(1821)
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                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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2812 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2854

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TYPE: DNA

FEATURE:

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Query Match 53.5%; Score 23; DB 4
Best Local Similarity 74.4%; Pred. No. 13;
Matches 29; Conservative 0; Mismatches
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US-09-949-016-15297
Sequence 15297, Application US/09949016
; Patent No. 6812339
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; LOCATION: (1)...(11752)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-11756
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Matches 43; Conservative
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6759236
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ORGANISM: Human
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Sequence 16898, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PELLING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-30

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 16898

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SEQ ID NO 16898
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Sequence 34, Application US/09109663

Sequence 34, Application US/09109663

Sequence 34, Application US/09109663

GENERAL INFORMATION:

APPLICANT: Total Value Chou

APPLICANT: Israel, Yelo

TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES

TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES

TITLE OF INVENTION: BFFICACIOUS ANTISENSE OLIGONUCLEOTIDES

CURRENT APPLICATION NUMBER: US/09/109,663

CURRENT FILING DATE: 1998-07-03

NUMBER OF SEQ ID NOS: 81

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 34

LENGTH: 3634
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Best Local Similarity 100.0%; Pred. No. 7.1e-08;
Matches 43; Conservative 0; Mismatches 0;
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US-09-949-016-16898
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US-09-376-774-5/c
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SQUENCE 11756, Application US/09949016

Faceure 11756, Application US/09949016

Faceure No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHIEMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOU3307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE PESSEQ FOR WINDOWS VERSION 4.0
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GENERAL INFORMATION:
APPLICANT: Fung, Yuen Kai
APPLICANT: Fung, Yuen Kai
APPLICANT: T'Ang, Anne
TITLE OF INVENTION: Methods To Enhance And Confine Expression
TITLE OP INVENTION: Of Genes
FILE REFERENCE: D6087;
CURRENT APPLICATION NUMBER: US/09/376,774
CURRENT FILING DATE: 2003-03-21
FRIOR RILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 5:
LENGTH: 10728
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
) OTHER INFORMATION: recombinant vector pDATH-TNP?
US-09-376-774-5
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 15297

LENGTH: 11865

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEX: misc. feature

105-09-949-016-15297
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Search completed: September 2, 2005, 18:55:20 Job time: 177.51 secs

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2, 2005, 15:27:57; Search time 198.034 Seconds (without alignments) 1421.994 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
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15: /cgn2_6/prodata/1/pubpna/USOP_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubpna/USOP_PUBCOMB.seq:*
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20: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
21: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
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27: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
28: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
28: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
28: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
28: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
28: /cgn2_6/prodata/1/pubpna/USOOP_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7338684 segs, 3274456166 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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43
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES		
Result No.	Score	* Query Match	* Query Match Length DB ]	038	ID	Description	
	43	100.0	43	9	9 US-09-801-371A-2	Sequence 2, Appli	
ر د	43	100.0	43	ტ	US-09-801-371A-6	Sequence 6, Appli	
m	43	100.0	20	σ	US-09-801-371A-8	Sequence 8, Appli	
4	43	100.0	81	σ	US-09-801-371A-7	Sequence 7, Appli	
S	43	100.0	104	σ	US-09-801-371A-1	Sequence 1, Appli	
9	43	100.0	104	σ	US-09-801-371A-5	Sequence 5, Appli	
7	43	100.0	787	18	US-10-356-308A-13	Sequence 13, Appl	

Sequence 9, Appli Sequence 120, Appli Sequence 120, Appli Sequence 1329, Appli Sequence 1329, Appli Sequence 1329, Appli Sequence 3, Appli Sequence 4, Appli Sequence 1901, Appli Sequence 1901, Appli Sequence 17, Appli Sequence 6, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18012, A Sequence 18012, A Sequence 6223, Appli Sequence 6223, Appli	
US-10-895-393-9 US-10-814-634A-5 US-10-814-634A-5 US-10-814-634A-5 US-10-172-118-501 US-10-172-118-501 US-10-172-118-501 US-10-172-118-19 US-10-272-411-4 US-10-272-411-4 US-10-272-411-4 US-10-272-411-9 US-10-272-411-9 US-10-272-687-1901 US-10-272-687-1901 US-10-272-687-1901 US-10-272-687-1901 US-10-272-687-1901 US-10-272-687-1901 US-10-273-680-1 US-10-273-680-3 US-10-770-970-1 US-10-770-970-1 US-10-770-970-1 US-10-770-970-1 US-10-770-970-1 US-10-770-970-1 US-10-770-970-1 US-10-770-970-1 US-10-770-602-623 US-10-770-602-6233 US-10-057-475-6223	
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## ALIGNMENTS

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US-09-801-371A-2

Sequence 2, Application US/09801371A

Sequence 2, Application US/09801371A

Sequence 2, Application US/09801371A

Sequence 2, Application US/09801371A

Sequence 3, Application US/09801371A

APPLICANT: Reampler, Raymond

APPLICANT: Barrous, Nayef

APPLICANT: Barrous, Nayef

APPLICANT: Barrous, Nayef

APPLICANT: Barrous, Nayef

APPLICANT: BARRANCE AA4084-PCT-USA-A 066031.0147

CURRENT FILIR OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES

FILE REPRENCE AA4084-PCT-USA-A 066031.0147

CURRENT FILIRO DATE: 2001-03-07

FRIOR PAPLICATION NUMBER: PCT WO 00/14255

FRIOR FILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 43

CURRENT Home sapiens

US-09-801-371A-2

Query March

Best Local Similarity 100.0%; Score 43; DB 9; Length 43;

Best Local Similarity 100.0%; Pred. No. 8e-08;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps
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1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43

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Sequence 1, Application US/09801371A

Sequence 1, Application US/09801371A

Patent No. US20020155569A1

GENERAL INFORMATION:
APPLICANT: Osman, Farhat
APPLICANT: Osman, Farhat
TITLE OF INVENTION: REQUIATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
FILE REFERENCE: A34084-FCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A

CURRENT APPLICATION NUMBER: US/09/801,371A

FRIOR PPLICATION NUMBER: PCT WO 00/14255

PRIOR PILING DATE: 1999-09-06

NUMBER OF SEQ ID NOS: 12
                                                                        APPLICANT: Jarrous, Nayef
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07.
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR PILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Osman, Farhat
APPLICANT: Osman, Farhat
APPLICANT: Jarrous, Nayef
APPLICANT: Ben-Asouli, Yitzhak
IIILE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
IIILE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
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Best Local Similarity 79.19
Matches 34; Conservative
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US-09-801-371A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
ORGANISM: Homo sapien
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Best Local Similarity
Matches 43; Conserv
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Faceut No. US2002015559A1
GENERAL INFORMATION
APPLICANT: Raempfer, Raymond
APPLICANT: Raempfer, Raymond
APPLICANT: Osman, Farhat
APPLICANT: Osman, Rayle
APPLICANT: Ben-Asouli, Yitzhak
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
TITLE OF INVENTION: MANIPULATION OF MANA SPLICING AND ITS USES
FILE REFERENCE: AA9084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,311A
CURRENT APPLICATION NUMBER: US/09/801,311A
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR PILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 50
                                                                                                                            Sequence 6, Application US/09801371A

Sequence 10, US2020155569A1

Sequence 10, US2020155569A1

September 10, US2020155569A1

APPLICANT: Kaempier, Raymond

APPLICANT: Osman, Farhat

APPLICANT: Osman, Farhat

TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH

TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES

FILE REFERENCE: A34084-PCT-USA-A 066031.0147

CURRENT APPLICATION NUMBER: US/09/801,371A

CURRENT FILING DATE: 2001-03-07

PRIOR PELLING DATE: 1999-09-06
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100.0%; Score 43; DB 9; Length 50;
Best Local Similarity 79.1%; Pred. No. 8e-08;
Matches 34; Conservative 9; Mismatches 0; Indels
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100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8e-08;
Matches 43; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapien
US-09-801-371A-8
                                                                                                           US-09-801-371A-6/c
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Length 104;

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APPLICANT: TRIFILLS, Panayiota
APPLICANT: TRIFILLS, Panayiota
APPLICANT: TROTA, Christopher R.
TITLE OF INVENTION: Methods and Agents for Screening for Compounds Capable of Modulat
TITLE OF INVENTION: Wethods and Agents for Screening for Compounds Capable of Modulat
TITLE OF INVENTION: Expression
FILE REFERENCE: 19025.012
CURRENT APPLICATION NUMBER: US/10/895,393
CURRENT FILING DATE: 2004-07-21
PRIOR APPLICATION NUMBER: E07/US04/01643
PRIOR FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 24
SOCTHARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 798
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; Publication No. US20040231007A1
; GENERAL INFORMATION:
; APPLICANT: CHENEVAL, Dominique
; APPLICANT: KASTELIC, Tania
; TITLE OF INVENTION: Affect Identifying Compounds Which
; TITLE OF INVENTION: Affect Stability of mRNA
; TITLE OF INVENTION: Affect Stability of mRNA
; TITLE OF INVENTION: Affect Stability of mRNA
; CURRENT APPLICATION NUMBER: US/10/814,634A
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FRAESEQ for Windows Version 4.0
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100.0%; Pred. No. 7.9e-08;
trive 0; Mismatches 0;
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100.0%; Pred. No. 7.9e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial
FRATURE:
OTHER INFORMATION: Synthetic Construct
US-10-895-393-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 120, Application US/10247671; Publication No. US20030194721A1; GENERAL INFORMATION:
APPLICANT: MAKITA, Thomas
APPLICANT: Shiffman, Dov
APPLICANT: Porter, Gordon, J.
              ROMFO, Charles M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
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Best Local Similarity 100.0
Matches 43; Conservative
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US-10-356-308A-13

Sequence 13, Application US/10356308A

Publication No. US20040039186A1

GENERAL INFORMATION:

APPLICANT: Tatake, Revati J.

APPLICANT: Barton, Randall Wilber

TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
FILE REPERENCE: 2003-01-31

FILE REPERENCE: 2003-01-31

PRIOR FILING DATE: 1990-02-27

PRIOR PLICATION NUMBER: US 69/032,297

PRIOR PLICATION NUMBER: US 60/039,266

PRIOR FILING DATE: 1997-02-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.0

SEQ ID NO 13

LENGTH: 787
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100.0%; Pred. No. 7.9e-08;
ive 0; Mismatches 0;
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OTHER INFORMATION: TNFa 3' untranslated region PUBLICATION INFORMATION.
AUTHORS: Nedwin, G.E., et al.
JOURNAL: Nucleic Acid Research
FILE REFERENCE: A34084-PCT-USA-A 066031.0147
CURRENT APPLICATION NUMBER: US/09/801,371A
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT WO 00/14255
PRIOR FILING DATE: 1999-09-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 43; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5
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US-10-641-643-1329
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CURRENT APPLICATION NUMBER: US/10/172,118
PRIOR APPLICATION WHERE: 60/380,770
PRIOR FILING DATE: 2002-05-14
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                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 561301CB1
US-10-247-671-120
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
FILE REFERENCE: PA-0050 US
CURRENT APPLICATION NUMBER: US/10/247,671
CURRENT TILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR APPLICATION NUMBER: 60/323,784
PRIOR APPLICATION 186
SEQ ID NOS: 186
SEQ ID NOS: 186
SEQ ID NOS: 186
SEQ ID NO 120
LENGTH: 1279
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DATABASE ACCESSION NUMBER: NM 000594
DATABASE ENTRY DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 501, Application US/10172118
Publication No. US20030224374A1
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Publication No. US20040058340A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer', Laura
APPLICANT: Van 'de Vijver, Marc
APPLICANT: Bernards, Rene
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Best Local Similarity 100.(
Matches 43; Conservative
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SEQ ID NO 501
LENGTH: 1585
                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-10-342-887-501
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APPLICANT:
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APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-186-999
CURRENT FILING DATE: 2003-01-15
CURRENT FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
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Publication No. US20040077003A1

GENERAL INFORMATION:

Susan G. Stuart

Jeffrey J. Sellhamer

TITLE OF INVENTION FOR THE DETECTION OF BLOOD CELL.

GENE EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1585;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-ANG-2003
CLASSIFICATION: <UNKNOWN>
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100.0%; Score 43; DB 18;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEB: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION UNMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UNMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                            Van 't Veer, Laura Johanna
Van de Vijver, Marc J.
Roberts, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEC ID NO: 1329:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 845-4166
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
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US-10-342-887-501
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DATABASE ACCESSION NUMBER: NCBI/ X01394.1
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APPLICANT: BODARY, SARAH C.
APPLICANT: BOLARK, HILLARY
APPLICANT: BRISDELL, HUNE
APPLICANT: STOKENELL, HUNE
APPLICANT: JACKMAN, JANET
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOO, WILLIAM, I.
APPLICANT: WOO, WILLIAM, I.
APPLICANT: WOO, WILLIAM, I.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
ITTLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION UNDER: US/10/370,715B
CURRENT PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
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100.0%; Score 43; DB 20; Length 1585;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0
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Publication No. US20030100068A1

GENERAL INFORMATION

APPLICANT: Barnes Jewish Hospital

APPLICANT: Lam, Jonathan

APPLICANT: Teitalbaum, Steven

TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF

FILE REFERENCE: 60019620-0202

CURRENT APPLICATION NUMBER: uS/10/272,411

CURRENT RILING DATE: 2002-10-15

PRIOR PLICATION NUMBER: 60/329,393

PRIOR PLICATION NUMBER: 60/329,393

PRIOR PLICATION NUMBER: 60/329,393

PRIOR PLICATION NUMBER: 5002-10-15

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin version 3.1
                                                    ; CLONE: 9339737
; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329
                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-370-715B-19
Sequence 19, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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ORGANISM: Homo sapiens
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TYPE: DNA
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LENGTH: 1643
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US-10-272-411-4
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DATABASE ENTRY DATE: 1995-03-21
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
DATABASE ENTRY DATE: 2002-05-01
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 1993-04-27
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI/
RELEVANT RESIDUES: (1)..(1643)
PUBLICATION INFORMATION:
DATABASE ENTRY DATE: 2002-08-01
RELEVANT RESIDUES: (1)..(1643)
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